

A:Molecule type: genomic RNA

A:Residues: 1-565 &lt;KAW&gt;

A:Cross-references: GB:M24727; GB:J04336; NID:G324000; PIDN:AAA43102.1; PID:G324001

C:Genetics:

A:Map position: segment 4

C:Superfamily: influenza virus hemagglutinin

C:Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond

F:1-16/Domain: signal sequence #status predicted &lt;SIG&gt;

F:17-344/Product: hemagglutinin HA1 #status predicted &lt;HA1&gt;

F:345-565/Product: hemagglutinin HA2 #status predicted &lt;HA2&gt;

F:535-551/Domain: transmembrane #status predicted &lt;TM1&gt;

F:18,23,37,53,78,180,300,498/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:29-481,67-292,79-91,154-488,296-320/Disulfide bonds: #status predicted

F:554,561,564/Binding site: palmitate (Cys) (covalent) #status predicted

Alignment Scores:

Pred. No.:	4,38e-142	Length:	565
Score:	1794.00	Matches:	333
Percent Similarity:	98.84%	Conservative:	7
Best Local Similarity:	96.80%	Mismatches:	4
Query Match:	93.83%	Indels:	0
DB:	1	Gaps:	0

US-10-826-929A-1 (1-1061) x HMIVE8 (1-565)

QY	30	ATGAAGACCAACCATTTATTTGATACCTACTGACCCATTTGGTCTACAGTCAAAACCCAAACC	89
DB	1	MetLysThrThrIleLeuLeuLeuLeuLeuThrHisTrpValTySerGlnAsnProThr	20
QY	90	AGTGGAAACACACAGCCACCATATGTCTGGGACACCAGTCAGTAGCAAAATGGAACATG	149
DB	21	SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu	40
QY	150	GTAAACAAATACATGATGACCAAAATGAGGTGACAAATGCTACTGAAATAGTTCAGAGC	209
DB	41	VallysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer	60
QY	210	ATTTCATAGGGAATATGCAACATCTCATATAAGTTCTAGATGGAAGAAATGGCACA	269
DB	61	IleSerIleGlyIleCysAsnAsnSerTyraGValLeuAspGlyArgAsnCysThr	80
QY	270	TTAATAGATGCAATGCTAGGAGACCCCACTGCTGATGCTTCCAGTATGAGAATGGGAC	329
DB	81	LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyrgluAsnTrpAsp	100
QY	330	CTCTTCATAGAAAGACGAGCGCTTTCAGCAATGCTACCCATATGACATCCCTGACTAT	389
DB	101	LeuPheIleGluArgSerSerAlaSerSerAsnCysTyProTyAspIleProAspTyr	120
QY	390	GCATCGCTCCGTCATCTGATCCTCAGCAACATTAAGATTCAGATGGAAGATTCACAGC	449
DB	121	AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe	140
QY	450	ACATGACAGAGGTGTCTACTCAAAACGGAAGTGGAGCTGCAAAAGGGGATCAGCCGAT	509
DB	141	ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysLysArgGlySerAlaAsp	160
QY	510	AGTTCTTTAGCGGACTGAATGGCTAAACAAATCTGGAACCTTACCCCAATGAT	569
DB	161	SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyProThrLeuAsn	180
QY	570	GTGACAAATCCCTAACAAATAAAATTCGACAAACTATACATCTGGGGGATTCATCCCG	629
DB	181	ValThrMetProAsnAsnAsnAsnPheAspLysLeuTyrlleTrpGlyIleHisPro	200
QY	630	AGTCAAAACACAGCAGACAGAAATGTATCATCCAAAGATCAGGACGAGTAACAGTCTCA	689
DB	201	SerSerAsnAsnGluGlnThrLysLeuTyrlleGlnGluSerGlyArgValThrValSer	220
QY	690	ACAAAAGAGTCAACAAACGATAGTCCCTATATCGGATCTAGACCGGTGAGGT	749
DB	221	ThrLysArgSerGlnGlnThrIleLeuProAsnIleGlySerArgProTrpValArgGly	240

QY	750	CAATCAGCAGGATAAGCATATCTACTGGACCATTTGTAACCTGGAGATATCTTAATGATA	809
DB	241	GlnSerGlyArgIleSerIleTyTrpThrIleValLysProGlyAspIleLeuIlele	260
QY	810	AACAGTAATGCAACTTAGTTGACCCCGGGGATATTTAAATTCGAAACAGGAAAGC	869
DB	261	AsnSerAsnGlyAsnLeuValAlaProArgGlyTyPheLysLeuArgThrGlyLysSer	280
QY	870	TCTGTAATGACATCAGATGACCCCATAGACATTTGTTGTCTGTAATGTATTACACCAAT	929
DB	281	SerValMetArgSerAspAlaProIleAspThrCysValSerGluCysIleThrProAsn	300
QY	930	GGAACATCCCAACACGACAAACCATTTCAAATGTGAACAAAGTTACATATGAAAATGC	989
DB	301	GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrglyLysCys	320
QY	990	CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA	1049
DB	321	ProLysTyrlleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu	340
QY	1050	AAGCAAAATCAGA	1061
DB	341	LysGlnIleArg	344

RESULT 5

HMIVE8

hemagglutinin precursor - influenza A virus (strain A/equine/Santiago/1/85 [H3N8])  
N:Contains: hemagglutinin HA1; hemagglutinin HA2

C:Species: influenza A virus

C:Date: 30-Sep-1990 #sequence\_revision 30-Sep-1990 #text\_change 16-Jul-1999

C:Accession: H34064

R:Kawaoka, Y.; Bean, W.J.; Webster, R.G.

Virology 169, 283-292, 1989

A:Title: Evolution of the hemagglutinin of equine H3 influenza viruses.

A:Reference number: A34064; MUID:89204899; PMID:2705299

A:Accession: H34064

A:Molecule type: genomic RNA

A:Residues: 1-565 &lt;KAW&gt;

A:Cross-references: GB:M24725; GB:J04336; NID:G324016; PIDN:AAA43110.1; PID:G324017

C:Genetics:

A:Map position: segment 4

C:Superfamily: influenza virus hemagglutinin

C:Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond

F:1-16/Domain: signal sequence #status predicted &lt;SIG&gt;

F:17-344/Product: hemagglutinin HA1 #status predicted &lt;HA1&gt;

F:345-565/Product: hemagglutinin HA2 #status predicted &lt;HA2&gt;

F:535-551/Domain: transmembrane #status predicted &lt;TM1&gt;

F:18,23,37,53,78,180,300,498/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:29-481,67-292,79-91,154-488,296-320/Disulfide bonds: #status predicted

F:554,561,564/Binding site: palmitate (Cys) (covalent) #status predicted

Alignment Scores:

Pred. No.:	6.55e-140	Length:	565
Score:	1768.00	Matches:	327
Percent Similarity:	97.97%	Conservative:	10
Best Local Similarity:	95.06%	Mismatches:	7
Query Match:	92.47%	Indels:	0
DB:	1	Gaps:	0

US-10-826-929A-1 (1-1061) x HMIVE8 (1-565)

QY	30	ATGAAGACCAACCATTTATTTGATACCTACTGACCCATTTGGTCTACAGTCAAAACCCAAACC	89
DB	1	MetLysThrThrIleLeuLeuLeuLeuThrHisTrpValTySerGlnAsnProThr	20
QY	90	AGTGGAAACACACAGCCACCATTTATGTCTGGGACACCAGTCAGTAGCAAAATGGAACATG	149
DB	21	SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu	40
QY	150	GTAAACAAATACATGATGACCAAAATGAGGTGACAAATGCTACTGAAATAGTTCAGAGC	209
DB	41	VallysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer	60





GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_r2p model

Run on: February 27, 2005, 18:15:54 ; Search time 48 Seconds  
(without alignments)

4253.583 Million cell updates/sec

Title: US-10-826-929A-1

Perfect score: 1912

Sequence: 1 agcaaaagcaggggatattt.....taccagaaaaagcaaatcaga 1061

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/cgn2\_1/USFTO.spool\_P/US10826929/runat\_27022005\_095243\_27596/app\_query.fasta\_1.1223  
-DB=PIR\_79 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10826929 @CN\_1.1\_53 @runat\_27022005\_095243\_27596 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR 79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1806	94.5	565	1 HMIVE9	hemagglutinin prec
2	1805	94.4	565	1 HMIVEE	hemagglutinin prec
3	1795	93.9	565	2 S33703	hemagglutinin - in
4	1794	93.8	565	1 HMIVET	hemagglutinin prec
5	1768	92.5	565	1 HMIVE7	hemagglutinin prec
6	1766	92.4	565	1 HMIVE8	hemagglutinin prec
7	1764	92.3	565	1 HMIVE6	hemagglutinin prec
8	1742	91.1	565	1 HMIVE5	hemagglutinin prec
9	1708	89.3	565	1 HMIVE1	hemagglutinin prec
10	1699	88.9	565	1 HMIVE2	hemagglutinin prec
11	1658	86.7	565	1 HMIVE4	hemagglutinin prec
12	1652	86.4	565	1 HMIVE3	hemagglutinin prec
13	1542.5	80.7	566	1 HMIVDU	hemagglutinin prec
14	1538	80.4	550	1 HMIVB9	hemagglutinin prec

15	1537	80.4	550	1 HMIV15	hemagglutinin prec
16	1537	80.4	550	1 HMIVS2	hemagglutinin prec
17	1536.5	80.4	566	1 HMIVH	hemagglutinin prec
18	1536	80.3	550	1 HMIV33	hemagglutinin prec
19	1533	80.2	550	2 JQ1153	hemagglutinin prec
20	1530	80.0	550	1 HMIV98	hemagglutinin prec
21	1528	79.9	550	2 JQ1155	hemagglutinin prec
22	1527.5	79.9	566	1 HMIVHA	hemagglutinin prec
23	1525	79.8	550	2 JQ1154	hemagglutinin prec
24	1524	79.7	550	1 HMIV77	hemagglutinin prec
25	1524	79.7	550	1 HMIV80	hemagglutinin prec
26	1514.5	79.2	550	1 HMIV21	hemagglutinin prec
27	1509	78.9	550	2 JQ1156	hemagglutinin prec
28	1501	78.5	550	1 HMIVS3	hemagglutinin prec
29	1479.5	77.4	566	1 HMIVHM	hemagglutinin prec
30	1477.5	77.3	566	1 HMIV6	hemagglutinin prec
31	1472	77.0	567	1 HMIVV	hemagglutinin prec
32	1428	74.7	550	1 HMIV86	hemagglutinin prec
33	1415	74.0	347	2 S52175	hemagglutinin - in
34	1414	74.0	347	2 S52188	hemagglutinin - in
35	1414	74.0	347	2 S52173	hemagglutinin - in
36	1411	73.8	347	2 S52174	hemagglutinin - in
37	1411	73.8	347	2 S52197	hemagglutinin - in
38	1410	73.7	331	2 JQ2377	hemagglutinin - in
39	1410	73.7	331	2 JQ2378	hemagglutinin - in
40	1410	73.7	347	2 S52198	hemagglutinin - in
41	1408	73.6	347	2 S52199	hemagglutinin - in
42	1406.5	73.6	330	2 JQ2375	hemagglutinin - in
43	1406	73.5	347	2 S52176	hemagglutinin - in
44	1404	73.4	347	2 S52183	hemagglutinin - in
45	1404	73.4	347	2 S52182	hemagglutinin - in

ALIGNMENTS

RESULT 1

HMIVE9

N:Contains: hemagglutinin precursor - influenza A virus (strain A/equine/Tennessees/5/85 [H3N8])  
C:Species: influenza A virus  
C>Date: 30-Sep-1990 #sequence\_revision 30-Sep-1990 #text\_change 16-Jul-1999  
C:Accession: I34064  
R:Kawoka, Y.; Bean, W.J.; Webster, R.G.  
Virology 169, 283-292, 1989

A:Title: Evolution of the hemagglutinin of equine H3 influenza viruses.  
A:Reference number: A34064; PMID:89204899; PMID:2705299  
A:Accession: I34064

A:Molecule type: genomic RNA

A:Residues: 1-565 <KAW>

A:Cross-references: GB:M24726; GB:J04336; NID:G324020; PIDN:AAA43112.1; PID:G324021

C:Genetics:

A:Map position: segment 4

C:Superfamily: influenza virus hemagglutinin

C:Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:17-34/Product: hemagglutinin HA1 #status predicted <HA1>  
F:345-565/Product: hemagglutinin HA2 #status predicted <HA2>  
F:535-551/Domain: transmembrane #status predicted <TM>

F:18,23,37,53,68,78,180,300,498/Binding site: carbohydrate (Asn) (covalent) #status pre

F:29-481,67-292,79-91,154-488,296-320/Disulfide bonds: #status predicted

F:554,561,564/Binding site: palmitate (Cys) (covalent) #status predicted

Alignment Scores:

Pred. No.: 4,358-143 Length: 565  
Score: 1806.00 Matches: 335  
Percent Similarity: 99.13% Conservative: 6  
Best Local Similarity: 97.38% Mismatches: 3  
Query Match: 94.46% Indels: 0  
DB: 1 Gaps: 0

US-10-826-929A-1 (1-1061) x HMIVE9 (1-565)

QY

30 ATGAAGACACACCAATTATTTTGTGACTACTGACCCATTGGTCTACAGTCAAAACCAACC 89

```
QY 270 TTATAGATGCAATGCTAGGAGACCCCACTGTGATGCTTCCAGTATGAGAATTGGGAC 329
Db 241 TTATAGATGCAATGCTAGGAGACCCCACTGTGATGCTTCCAGTATGAGAATTGGGAC 300
QY 330 CTCCTCATAGAAAGACGAGCGCTTTAGCAATGCTACCCATATGACATCCCTGACTAT 389
Db 301 CTCCTCATAGAAAGACGAGCGCTTTAGCAATGCTACCCATATGACATCCCTGACTAT 360
QY 390 GCATCGCTCCGCTCCATTTGTAGCATCCTCAGGAACATTAGAAATTCACAGCAGAGGGATTC 449
Db 361 GCATCGCTCCGCTCCATTTGTAGCATCCTCAGGAACATTAGAAATTCACAGCAGAGGGATTC 420
QY 450 ACATGGACAGGTGTCACTCAAAACGGAAGAGTGGAGCCTGCAAAAGGGGATCAGCCCGAT 509
Db 421 ACATGGACAGGTGTCACTCAAAACGGAAGAGTGGATCCTGCAAAAGGGGATCAGCCCGAT 480
QY 510 AGTTCTTTTAGCCGACTGAATTTGGCTAACAAAATCTGGAAATCTTTACCCCAATTTGAAT 569
Db 481 AGTTCTTTTAGCCGACTGAATTTGGCTAACAGAATCTGGAAATCTTTACCCCAATTTGAAT 540
QY 570 GTGACAAATGCTTAACAATAAATTTGACAAACTATACATCTGGGGGATTCATCACCAG 629
Db 541 GTGACAAATGCTTAACAATAAATTTGACAAACTATACATCTGGGGGATTCATCACCAG 600
QY 630 AGCTCAAAACAGCAGACAGAAATTTGATCCAGAAATCAGGACGAGTAAACAGTCTCA 689
Db 601 AGCTCAAAACAGCAGACAGAAATTTGATCCAGAAATCAGGACGAGTAAACAGTCTCA 660
QY 690 ACAAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCCGTGGGTTAGGGGT 749
Db 661 ACAAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCCGTGGGTTAGGGGT 720
QY 750 CAATCAGGCGAGTAAGCATATACGACCATTTGTAACCTGGAGATATCCTAATGATA 809
Db 721 CAATCAGGCGAGTAAGCATATACGACCATTTGTAACCTGGAGATATCCTAATGATA 780
QY 810 AACAGTAATGGCAACTTAGTTGCACCGCGGGATATTTTAAATTTGAAAACAGGGAAGC 869
Db 781 AACAGTAATGGCAACTTAGTTGCACCGCGGGATATTTTAAATTTGAAAACAGGGAAGC 840
QY 870 TCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTCTGATGTATTAACCAAT 929
Db 841 TCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTCTGATGTATTAACCAAT 900
QY 930 GGAAGCATCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACATATGGAATGC 989
Db 901 GGAAGCATCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACATATGGAATGC 960
QY 990 CCCAGTATATCAGGCAAAACACTTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1049
Db 961 CCCAGTATATCAGGCAAAACACTTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1020
QY 1050 AAGCAATCAGA 1061
Db 1021 AAGCAATCAGA 1032
```

Search completed: March 1, 2005, 08:24:20  
Job time : 2066 secs

## RESULT 14

US-10-065-133A-9

; Sequence 9, Application US/10065133A

; Publication No. US20030199074A1

; GENERAL INFORMATION:

; APPLICANT: Dowling, Patricia W.

; APPLICANT: Youngner, Julius S.

; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES

; FILE REFERENCE: EQ-1-C2-1

; CURRENT APPLICATION NUMBER: US/10/065,133A

; CURRENT FILING DATE: 2002-12-10

; PRIOR APPLICATION NUMBER: PCT/US99/18583

; PRIOR FILING DATE: 1999-08-12

; PRIOR APPLICATION NUMBER: 09/133,921

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 9

; LENGTH: 1695

; TYPE: DNA

; ORGANISM: Equine influenza virus H3N8

US-10-065-133A-9

Query Match 94.6%; Score 1003.2; DB 16; Length 1695;

Best Local Similarity 98.3%; Pred. No. 3.9e-269;

Matches 1014; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

```
QY 30 ATGAAGACAAACCAATTTTGTATCTACTGACCCATTTGGTCTACAGTCAAAACCCAAACC 89
DB 1 ATGAAGACAAACCAATTTTGTATCTACTGACCCATTTGGTCTACAGTCAAAACCCAAACC 60
QY 90 AGTGGAAACAAACACAGCCATTTATCTGGGACACCATGTCAGTACCAATGAAATG 149
DB 61 AGTGGAAACAAACACAGCCATTTATCTGGGACACCATGTCAGTACCAATGAAATG 120
QY 150 GTAAAAACAATACTGATGACCAAAATGAGGTGACCAAAATGCTACTGAAATGTTTCAGAGC 209
DB 121 GTAAAAACAATACTGATGACCAAAATGAGGTGACCAAAATGCTACTGAAATGTTTCAGAGC 180
QY 210 ATTTCAATAGGAAATATGCAACAACTCATATATAAGTTCTAGATGGAAGAAATTCACAC 269
DB 181 ATTTCAATAGGAAATATGCAACAACTCATATATAAGTTCTAGATGGAAGAAATTCACAC 240
QY 270 TTAATAGATGCAATGCTAGGAGACCCCACTGATGCTCTCCAGATGAGAAATTCGGAC 329
DB 241 TTAATAGATGCAATGCTAGGAGACCCCACTGATGCTCTCCAGATGAGAAATTCGGAC 300
QY 330 CTCTTCATAGAAAGACGCGCTTTTTCAGCAATTTGCTACCCATATGACATCCCTGACTAT 389
DB 301 CTCTTCATAGAAAGACGCGCTTTTTCAGCAATTTGCTACCCATATGACATCCCTGACTAT 360
QY 390 GCATCCTCGGTCCATTTAGCATCTCTAGGAACATTTAGAAATTCACAGAGGGAATTC 449
DB 361 GCATCCTCGGTCCATTTAGCATCTCTAGGAACATTTAGAAATTCACAGAGGGAATTC 420
QY 450 ACATGACAGGTGTCTACTCAAAACGGAAGAGTGGAGCTGCAAAAGGGGATCAGCCGAT 509
DB 421 ACATGACAGGTGTCTACTCAAAACGGAAGAGTGGAGCTGCAAAAGGGGATCAGCCGAT 480
QY 510 AGTTTCTTTTAGCCGACTGAATTTGGCTTAAACAAATCTGGAATCTTTTACCCCAATTTGAAT 569
DB 481 AGTTTCTTTTAGCCGACTGAATTTGGCTTAAACAAATCTTTTACCCCAATTTGAAT 540
QY 570 GTGCAATGCTTAAACAAATTTTTCGAACTATATCATCTGGGGGATTCATCACCCG 629
DB 541 GTGCAATGCTTAAACAAATTTTTCGAACTATATCATCTGGGGGATTCATCACCCG 600
QY 630 AGCTCAACCAACAGCAGACAGATTTGTATCTCCAGATCAGGAGTAAACAGTCTCA 689
DB 601 AGCTCAACCAACAGCAGACAGATTTGTATCTCCAGATCAGGAGTAAACAGTCTCA 660
```

```
QY 690 ACAAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGGTAGGGT 749
DB 661 ACAAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGGTCAGGGT 720
QY 750 CAATCAGGAGGATAGGATATATCTGACCATTTGTAACCTGAGATATCTTAATGATA 809
DB 721 CAATCAGGAGGATAGGATATATCTGACCATTTGTAACCTGAGATATCTTAATGATA 780
QY 810 AACAGTAATGGCAACTTAGTTGACCGCGGGGATATTTTAAATTTGAAAAACAGGAAAGC 869
DB 781 AACAGTAATGGCAACTTAGTTGACCGCGGGGATATTTTAAATTTGAAAAACAGGAAAGC 840
QY 870 TCTGTAATGAGATCAGATGACCATGACCATTTGTTGTCTGTAATGTTATACCAAAAT 929
DB 841 TCTGTAATGAGATCAGATGACCATGACCATTTGTTGTCTGTAATGTTATACCAAAAT 900
QY 930 GGAAGCATCCCAACGACAAACCATTTTCAAAATGTAACAAAGTTACATATGAAATGTC 989
DB 901 GGAAGCATCCCAACGACAAACCATTTTCAAAATGTAACAAAGTTACATATGAAATGTC 960
QY 990 CCCAAGTATATCAGGCAAAACCACTTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1049
DB 961 CCCAAGTATATCAGGCAAAACCACTTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1020
QY 1050 AAGCAAAATCAGA 1061
DB 1021 AAGCAAAATCAGA 1032
```

## RESULT 15

US-10-434-811A-9

; Sequence 9, Application US/10434811A

; Publication No. US20040022809A1

; GENERAL INFORMATION:

; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher

; APPLICANT: Education

; APPLICANT: Dowling, Patricia W.

; APPLICANT: Youngner, Julius S.

; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES

; FILE REFERENCE: EQ-1-CJ-PUS-1

; CURRENT APPLICATION NUMBER: US/10/434,811A

; CURRENT FILING DATE: 2003-05-08

; PRIOR APPLICATION NUMBER: PCT/US99/18583

; PRIOR FILING DATE: 1999-08-12

; PRIOR APPLICATION NUMBER: 09/133,921

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 9

; LENGTH: 1695

; TYPE: DNA

; ORGANISM: Equine influenza virus H3N8

US-10-434-811A-9

## Query Match

94.6%; Score 1003.2; DB 17; Length 1695;

Best Local Similarity 98.3%; Pred. No. 3.9e-269;

Matches 1014; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

```
QY 30 ATGAAGACAAACCAATTTTGTATCTACTGACCCATTTGGTCTACAGTCAAAACCCAAACC 89
DB 1 ATGAAGACAAACCAATTTTGTATCTACTGACCCATTTGGTCTACAGTCAAAACCCAAACC 60
QY 90 AGTGGAAACAAACACAGCCATTTATCTGGGACACCATGTCAGTACCAATGAAATG 149
DB 61 AGTGGAAACAAACACAGCCATTTATCTGGGACACCATGTCAGTACCAATGAAATG 120
QY 150 GTAAAAACAATACTGATGACCAAAATGAGGTGACCAAAATGCTACTGAAATGTTTCAGAGC 209
DB 121 GTAAAAACAATACTGATGACCAAAATGAGGTGACCAAAATGCTACTGAAATGTTTCAGAGC 180
QY 210 ATTTCAATAGGAAATATGCAACAACTCATATATAAGTTCTAGATGGAAGAAATTCACAC 269
DB 181 ATTTCAATAGGAAATATGCAACAACTCATATATAAGTTCTAGATGGAAGAAATTCACAC 240
```

Db 421 ACATGGACAGGTGTCACTCAAAACGGAAGAGTGGATCCTGCAAAAGGGAATCAGCCGAT 480  
QY 510 AGTTCTTTAGCCGACTGAATTTGGCTTAACAAAATCTGGAATCTTTACCCCAATTTGAAT 569  
Db 481 AGTTCTTTAGCCGACTGAATTTGGCTTAACAGAACTCTGGAATCTTTACCCCAATTTGAAT 540  
QY 570 GTGCAATGCTTAACAAATAAAATTTGCAAAACTATATACATCTGGGGGATTCATCACC 629  
Db 541 GTGCAATGCTTAACAAATAAAATTTGCAAAACTATATACATCTGGGGGATTCATCACC 600  
QY 630 AGCTCAACCAACAGCAGAGAGAAATTTGATCATCAAGAAATCAGGACGAGTAACAGTCTCA 689  
Db 601 AGCTCAACCAACAGCAGAGAGAAATTTGATCATCAAGAAATCAGGACGAGTAACAGTCTCA 660  
QY 690 ACAAAGAGGTCAACAAACGATAGTCCCTTAATATCGGATCTAGACCGTGGGTAGGGGT 749  
Db 661 ACAAAGAGGTCAACAAACATATATCCCTAATCTGGATCTAGACCGTGGGTAGGGGT 720  
QY 750 CAATCAGGAGGATAGCATATATCTGGACCAATTTGTAACCTGGAGATATCCTAATGATA 809  
Db 721 CAATCAGGAGGATAGCATATATCTGGACCAATTTGTAACCTGGAGATATCCTAATGATA 780  
QY 810 AACAGTAATGGCACTTAGTTCGACCGCGGGGATATTTAAATTTGAAAACAGGGAAGC 869  
Db 781 AACAGTAATGGCACTTAGTTCGACCGCGGGGATATTTAAATTTGAAAACAGGGAAGC 840  
QY 870 TCTGTAATGAGATCAGATCAGCCACCATAGACATTTGTTGTCGTGAATGTATATACCAAT 929  
Db 841 TCTGTAATGAGATCAGATCAGCCACCATAGACATTTGTTGTCGTGAATGTATATACCAAT 900  
QY 930 GGAAGCATCCCAACGACAAACCAATTTCAAAATGTGAACAAAGTTTACATATGAAAAATGC 989  
Db 901 GGAAGCATCCCAACGACAAACCAATTTCAAAATGTGAACAAAGTTTACATATGAAAAATGC 960  
QY 990 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1049  
Db 961 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1020  
QY 1050 AAGCAATCAGA 1061  
Db 1021 AAGCAATCAGA 1032

RESULT 13  
US-10-872-014-12  
; Sequence 12, Application US/10872014  
; Publication No. US20040234553A1  
; GENERAL INFORMATION:  
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher Edu  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-CI-PUS-1  
; CURRENT APPLICATION NUMBER: US/10/872,014  
; CURRENT FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 10/434,811  
; PRIOR FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: 09/762,861  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 12  
; LENGTH: 1695  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
US-10-872-014-12

Query Match 94.7%; Score 1004.8; DB 18; Length 1695;  
Best Local Similarity 98.4%; Pred. No. 1.4e-269;

Matches 1015; Conservative 0; Mismatches 17; Indels 0; Gaps 0;  
QY 30 ATGAAGACAAACATTTATTTTGTGATCTACTGACCCATCTGGGTCTACAGTCAAAACCCCAACC 89  
Db 1 ATGAAGACAAACATTTATTTTGTGATCTACTGACCCATCTGGGTCTACAGTCAAAACCCCAACC 60  
QY 90 AGTGGAAACAAACAGCCACATTTATGCTCTGGGACACCATGCAAGTACCAATGGAACATTTG 149  
Db 61 AGTGGAAACAAACAGCCACATTTATGCTCTGGGACACCATGCAAGTACCAATGGAACATTTG 120  
QY 150 GTAAAAACAACTGATGACCAATTTGAGGTGCAAAATGCTACTGAAATTTAGTTTCAGAGC 209  
Db 121 GTAAAAACAACTGATGACCAATTTGAGGTGCAAAATGCTACTGAAATTTAGTTTCAGAGC 180  
QY 210 ATTTCAATAGGAAATATGCAACAACTCATATAAGTTCTAGATGGAAGAAATTTGCACA 269  
Db 181 ATTTCAATAGGAAATATGCAACAACTCATATAAGTTCTAGATGGAAGAAATTTGCACA 240  
QY 270 TTAATAGATGCAATGCTAGGAGACCCCACTGTGTGATGCTTTCCAGTATGAGAAATTTGGGAC 329  
Db 241 TTAATAGATGCAATGCTAGGAGACCCCACTGTGTGATGCTTTCCAGTATGAGAAATTTGGGAC 300  
QY 330 CTCCTTATAGAAAGAGCAGCGCTTTTTCAGCAATTTGCTACCCATATGACATCCCTGACTAT 389  
Db 301 CTCCTTATAGAAAGAGCAGCGCTTTTTCAGCAATTTGCTACCCATATGACATCCCTGACTAT 360  
QY 390 GCATCGCTCCCGTCCATTTGATAGCATCTTCAGCAATTTAGAAATTTCAACAGCAGGGAATTC 449  
Db 361 GCATCGCTCCCGTCCATTTGATAGCATCTTCAGCAATTTAGAAATTTCAACAGCAGGGAATTC 420  
QY 450 ACATGGACAGGTGTCACTCAAAACGGAAGAGTGGAGCTTCGCAAAAGGGGATCAGCCGAT 509  
Db 421 ACATGGACAGGTGTCACTCAAAACGGAAGAGTGGATCCTCTGCAAAAGGGAATCAGCCGAT 480  
QY 510 AGTTCTTTAGCCGACTGAATTTGGCTTAACAAAATCTGGAATCTTTACCCCAATTTGAAT 569  
Db 481 AGTTCTTTAGCCGACTGAATTTGGCTTAACAAAATCTGGAATCTTTACCCCAATTTGAAT 540  
QY 570 GTGCAATGCTTAACAAATAAAATTTGCAAAACTATATACATCTGGGGGATTCATCACC 629  
Db 541 GTGCAATGCTTAACAAATAAAATTTGCAAAACTATATACATCTGGGGGATTCATCACC 600  
QY 630 AGCTCAACCAACAGCAGACAGAAATTTGATCAATCCAAAGATCAGGACGAGTAACAGTCTCA 689  
Db 601 AGCTCAACCAACAGCAGACAGAAATTTGATCAATCCAAAGATCAGGACGAGTAACAGTCTCA 660  
QY 690 ACAAAGAGGTCAACAAACGATAGTCCCTTAATATCGGATCTAGACCGTGGGTAGGGGT 749  
Db 661 ACAAAGAGGTCAACAAACCAATTTATCCCTAATCTAGACCGTGGGTAGGGGT 720  
QY 750 CAATCAGGAGGATAGCATATATCTGGACCAATTTGTAACCTGGAGATATCCTAATGATA 809  
Db 721 CAATCAGGAGGATAGCATATATCTGGACCAATTTGTAACCTGGAGATATCCTAATGATA 780  
QY 810 AACAGTAATGGCACTTAGTTCGACCGCGGGGATATTTAAATTTGAAAACAGGGAAGC 869  
Db 781 AACAGTAATGGCACTTAGTTCGACCGCGGGGATATTTAAATTTGAAAACAGGGAAGC 840  
QY 870 TCTGTAATGAGATCAGATGACCAATTTGAGTGTGCTGATGATGATATACCAAT 929  
Db 841 TCTGTAATGAGATCAGATGACCAATTTGAGTGTGCTGATGATGATATACCAAT 900  
QY 930 GGAAGCATCCCAACGACAAACCAATTTCAAAATGTGAACAAAGTTTACATATGAAAAATGC 989  
Db 901 GGAAGCATCCCAACGACAAACCAATTTCAAAATGTGAACAAAGTTTACATATGAAAAATGC 960  
QY 990 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1049  
Db 961 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1020  
QY 1050 AAGCAATCAGA 1061  
Db 1021 AAGCAATCAGA 1032

```
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-434-811A-12

Query Match      94.7%; Score 1004.8; DB 17; Length 1695;
Best Local Similarity 98.4%; Pred. No. 1.4e-269;
Matches 1015; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 30 ATGAAGACACACACACACACACATTTTGTGATCTACTGACCCATTTGGGTCTTACAGTCAAAACCCAAACC 89
Db 1 ATGAAGACACACACACACACACATTTTGTGATCTACTGACCCATTTGGGTCTTACAGTCAAAACCCAAACC 60

QY 90 AGTGGAAACACACACACACACATTTATGCTGGGACACATGTCAGTCAAAATGGAACATTTG 149
Db 61 AGTGGAAACACACACACACATTTATGCTGGGACACATGTCAGTCAAAATGGAACATTTG 120

QY 150 GTAAAAACAATACTGATGACCAAAATTTAGGTGACAAATGCTACTGCAATTTAGTTTCAGAGC 209
Db 121 GTAAAAACAATACTGATGACCAAAATTTAGGTGACAAATGCTACTGCAATTTAGTTTCAGAGC 180

QY 210 ATTTCAATAGGGAATAATATGCAAACTCATATATAAGTTTCTAGATGGAAGAAATTCACAC 269
Db 181 ATTTCAATAGGGAATAATATGCAAACTCATATATAAGTTTCTAGATGGAAGAAATTCACAC 240

QY 270 TTAAATAGATGCAATGCTAGAGACCCCACTGTGTGATGTTCTTCCAGTATGAGAATTTGGGAC 329
Db 241 TTAAATAGATGCAATGCTAGAGACCCCACTGTGTGATGTTCTTCCAGTATGAGAATTTGGGAC 300

QY 330 CTCTTCATAGAAAGACGACGCTTTTACGAAATTTGCTTACCAATTCATGACATCCCTGACTAT 389
Db 301 CTCTTCATAGAAAGACGACGCTTTTACGAAATTTGCTTACCAATTCATGACATCCCTGACTAT 360

QY 390 GCATCGCTCCGGTCCCAATTTAGTATGCTCCTCAGGAACATTTAGAAATTCACAGAGGGATTC 449
Db 361 GCATCGCTCCGGTCCCAATTTAGTATGCTCCTCAGGAACATTTAGAAATTCACAGAGGGATTC 420

QY 450 ACATGACAGGTGCTCACTCAAAACGGAAGTGGATCTTGCAGAACTCTTACCCCAATTTGAAT 509
Db 421 ACATGACAGGTGCTCACTCAAAACGGAAGTGGATCTTGCAGAACTCTTACCCCAATTTGAAT 480

QY 510 AGTTTCTTTAGCCGACTGAATTTGGCTAAACAAATCTTGAACCTCTTACCCCAATTTGAAT 569
Db 481 AGTTTCTTTAGCCGACTGAATTTGGCTAAACAAATCTTGAACCTCTTACCCCAATTTGAAT 540

QY 570 GTGCAATGCTTAACAAATAAATTTTGAACAACTATATATCTTGGGGATTTCTACCCCG 629
Db 541 GTGCAATGCTTAACAAATAAATTTTGAACAACTATATATCTTGGGGATTTCTACCCCG 600

QY 630 AGCTCAACCAACAGCAGACAGATTTCTATCCAGAAATTCAGACAGTAAACAGTCTCA 689
Db 601 AGCTCAACCAACAGCAGACAGATTTCTATCCAGAAATTCAGACAGTAAACAGTCTCA 660

QY 690 ACAAAAAGAGTCAACAAACGATAGTCCCTAAATTCGGATCTAGACCGTGGGTAGGGGT 749
Db 661 ACAAAAAGAGTCAACAAACGATAGTCCCTAAATTCGGATCTAGACCGTGGGTAGGGGT 720

QY 750 CAATCAGCGAGGATAAGCATATATCTGGAACATTTGTAAACCTGGAGATATCTTAATGATA 809
Db 721 CAATCAGCGAGGATAAGCATATATCTGGAACATTTGTAAACCTGGAGATATCTTAATGATA 780

QY 810 AACAGTAATGCGCACTTAGTTGACCCGGGGATTTTAAATTTGAAAAACAGGAGAAAGC 869
Db 781 AACAGTAATGCGCACTTAGTTGACCCGGGGATTTTAAATTTGAAAAACAGGAGAAAGC 840

QY 870 TCTGTAATGAGATCAGATGCACCCATAGACATTTTGTGTCTGAAATGTTATACACCAAAAT 929
```

```
RESULT 12
US-10-734-373-12
; Sequence 12, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/734,373
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-734-373-12
```

```
Query Match      94.7%; Score 1004.8; DB 18; Length 1695;
Best Local Similarity 98.4%; Pred. No. 1.4e-269;
Matches 1015; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 30 ATGAAGACACACACATTTTGTGATCTACTGACCCATTTGGGTCTTACAGTCAAAACCCAAACC 89
Db 1 ATGAAGACACACATTTTGTGATCTACTGACCCATTTGGGTCTTACAGTCAAAACCCAAACC 60

QY 90 AGTGGAAACACACACACACATTTATGCTGGGACACATGTCAGTCAAAATGGAACATTTG 149
Db 61 AGTGGAAACACACACACACATTTATGCTGGGACACATGTCAGTCAAAATGGAACATTTG 120

QY 150 GTAAAAACAATACTGATGACCAAAATTTAGGTGACAAATGCTACTGCAATTTAGTTTCAGAGC 209
Db 121 GTAAAAACAATACTGATGACCAAAATTTAGGTGACAAATGCTACTGCAATTTAGTTTCAGAGC 180

QY 210 ATTTCAATAGGGAATAATATGCAAACTCATATATAAGTTTCTAGATGGAAGAAATTCACAC 269
Db 181 ATTTCAATAGGGAATAATATGCAAACTCATATATAAGTTTCTAGATGGAAGAAATTCACAC 240

QY 270 TTAAATAGATGCAATGCTAGAGACCCCACTGTGTGATGTTCTTCCAGTATGAGAATTTGGGAC 329
Db 241 TTAAATAGATGCAATGCTAGAGACCCCACTGTGTGATGTTCTTCCAGTATGAGAATTTGGGAC 300

QY 330 CTCTTCATAGAAAGACGACGCTTTTACGAAATTTGCTTACCAATTCATGACATCCCTGACTAT 389
Db 301 CTCTTCATAGAAAGACGACGCTTTTACGAAATTTGCTTACCAATTCATGACATCCCTGACTAT 360

QY 390 GCATCGCTCCGGTCCCAATTTAGTATGCTCCTCAGGAACATTTAGAAATTCACAGAGGGATTC 449
Db 361 GCATCGCTCCGGTCCCAATTTAGTATGCTCCTCAGGAACATTTAGAAATTCACAGAGGGATTC 420

QY 450 ACATGACAGGTGCTCACTCAAAACGGAAGTGGATCTTGCAGAACTCTTACCCCAATTTGAAT 509
```

Qy	601	AACTATACATCTGGGGGATTCATCACCCGAGGCTCAAAACCAACAGCAGACAGAAATTGTACA	660
Db	601	AACTATACATCTGGGGGATTCATCACCCGAGGCTCAAAACCAAGAGCAGACAAAATTGTACA	660
Qy	661	TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAGAAGTCAACAAAACATAGTCCCTA	720
Db	661	TCCAAGNATCGGACGAGTAAACAGTCTCAACAAAAGNAGTCAACAAACATTAATCCCTA	720
Qy	721	ATATCGGATCTAGACCGTGGGTAGGGGTCAATCAGGCAGGATAAGCATATATCTGGACCA	780
Db	721	ACATCGGATCTAGACCGCGGTGAGGGGTCAATCAGGCAGGATAAGCATATATCTGGACCA	780
Qy	781	TTGTAAAACTGTGAGATATCCTTAATGATAACAGTAATGCAACTTAGTTGACCCGCGG	840
Db	781	TTGTAAAACTGTGAGATATCCTTAATGATAACAGTAATGCAACTTAGTTGACCCGCGG	840
Qy	841	GATATTTTAAATTGAAAACAGGGAAAAGCTCTGTAAATGAGATCAGATGCACCCATAGACA	900
Db	841	GATATTTTAAATTGAAAACAGGGAAAAGCTCTGTAAATGAGATCAGATGCACCCATAGACA	900
Qy	901	TTTGTGTGCTGATGTATTTACACCAATGGAAGCATCCCCACGACAAACCAATTTCAA	960
Db	901	TTTGTGTGCTGATGTATTTACACCAATGGAAGCATCCCCACGACAAACCAATTTCAA	960
Qy	961	ATGTGAACAAAGTTTACATATGGAATAATGCCCAAGTATATCAGGCACAAAACATTTAAAGC	1020
Db	961	ATGTGAACAAAGTTTACATATGGAATAATGCCCAAGTATATCAGGCACAAAACATTTAAAGC	1020
Qy	1021	TGGCCACTGGGATGAGGAATATATCCAGAAAAGCAAAATCAGA	1061
Db	1021	TGGCCACTGGGATGAGGAATGTATCCAGAAAAGCAAAATCAGA	1061

RESULT 10 ;  
US-10-065-133A-12 ;  
; Sequence 12, Application US/10065133A  
; Publication No. US20030199074A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES

Query Match 94.7%; Score 1004.8; DB 16; Length 1695;  
Best Local Similarity 98.4%; Pred. No. 1.4e-269;  
Matches 1015; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

	Qy	30	ATGAAGACAACCAATTATTTTGATACTACTGACCATTGGGTCTACAGTCAAACCCAAACC	89
	Dz	1	ATGAAGACAACCAATTATTTTGATACTACTGACCATTGGGTCTACAGTCAAACCCAAACC	60
	Qy	90	AGTGGAAACAACACAGGCCAATTATGTCTCGGCACCATTCAGTAGCAAAATGGAACATTG	149
	Dz	61	AGTGGCAACAACACAGGCCAATTATGTCTCGGCACCATTCAGTAGCAAAATGGAACATTG	120
	Qy	150	GTA AAAAACAA TAA CTG ATG A TC C CA AA TT G AG TG A C AA AT GT C TA CT GA NT TAG TT CA GA GC	209
	Dz	121	GTA AAAAACAA TAA CTG ATG A TC C CA AA TT G AG TG A C AA AT GT C TA CT GA NT TAG TT CA GA GC	180
	Qy	210	ATTTCAATAGGGAANAATATGCAACA CT CAT ATA AA AGT TCT AG A NT GG A A GA A ATT TG CA CA	269

QY	61	CCCAATTGGGTCTACAGTCAAAACCCAAACCCAGTGGAAACAACAGCCCACTATTCTCTGG	120
Db	61	CCCAATTGGGTCTACAGTCAAAACCCAAACCCAGTGGCAACAACAGCCCACTATTCTCTGG	120
QY	121	GACACCATCAGTAGCAAAATGGAACATTTGGTAAAAACAATACTGATGACCAAAATTTGAGG	180
Db	121	GACACCATCAGTAGCAAAATGGAACATTTGGTAAAAACAATACTGATGACCAAAATTTGAGG	180
QY	181	TGACAAATGCTACTGAAATTAGTTTCAGAGCATTTTCAATAGGGGAAAAATATGCAACAAC	240
Db	181	TGACAAATGCTACTGAAATTAGTTTCAGAGCATTTTCAATAGGGGAAAAATATGCAACAAC	240
QY	241	ATAAAGTTCTAGATGGAAGAAATTTGACACATTAATAGATGCAATGCTAGGAGACCCCACT	300
Db	241	ATAGAGTTCTAGATGGAAGAAATTTGACACATTAATAGATGCAATGCTAGGAGACCCCACT	300
QY	301	GTGATGCTTTCCAGTATGAAATTTGGGACCTCTTTCATAGAAAGAACGACGCGCTTTTCAGCA	360
Db	301	GTGATGCTTTTCAGTATGAAATTTGGGACCTCTTTCATAGAAAGAACGACGCGCTTTTCAGCA	360
QY	361	ATTGTACCCATATGACATCCCTGACTATGCAATCGCTCCGGTCCATTTAGCATCTCTGAG	420
Db	361	GTGTCTAACCAATGACATCCCTGACTATGCAATCGCTCCGGTCCATTTAGCATCTCTCAG	420
QY	421	GAACTATTAGATTTACAGCAGAGGGATTCACATGGACAGGTGTCACTCAAAAACGGAAGAA	480
Db	421	GAACTATTGGAATTTACAGCAGAGGGATTCACATGGACAGGTGTCACTCAAAAACGGAAGAA	480
QY	481	GTGGAGCCTGCAAAAAGGGATCAGCCGATAGTTTCTTTTAGCCGACTGAATTCGGCTAA	540
Db	481	GTGGATCCTGCAAAAAGGGATCAGCCGATAGTTTCTTTTAGCCGACTGAATTCGGCTAA	540
QY	541	AATCTGGAAACTCTTACCCACATTCGAATGTGCAANTGCTTACCAATAAAATTTTCGACA	600
Db	541	AATCTGGAAACTCTTACCCACATTCGAATGTGCAANTGCTTACCAATAAAATTTTCGACA	600
QY	601	AACATATACATCTGGGGGATTCATCACCCGAGCTCAAAACCAACAGCAGACAGAAATTGTACA	660
Db	601	AACATATACATCTGGGGGATTCATCACCCGAGCTCAAAACCAACAGCAGACAGAAATTGTACA	660
QY	661	TCCAAGATCAGACCGAGTAAACAGTCTCAACAAAAGAGTCAACAAACGATAGTCCCTTA	720
Db	661	TCCAAGAACTCGGACCGAGTAAACAGTCTCAACAAAAGAGTCAACAAACGATAGTCCCTTA	720
QY	721	ATATCGGATCTAGACCGTGGGTTAGGGGTCAATCAGCGAGGATAAGCATATATCTGACCA	780
Db	721	ACATCGGATCTAGACCGCGGGTCAGGGGTCAATCAGCGAGGATAAGCATATATCTGACCA	780
QY	781	TTGTAAACCTCGAGATATCTTAATGATAACAGTAATGGCACTTAGTTGACACCGGGG	840
Db	781	TTGTAAACCTCGGAGTATCTTAATGATAACAGTAATGGCACTTAGTTGACACCGGGG	840
QY	841	GATATTTTAAATTTGAAAACAGGAAAAGCTCTCTGAATAGATCAGATGCAACCCATAGACA	900
Db	841	GATATTTTAAATTTGAAAACAGGAAAAGCTCTCTGAATAGATCAGATGCAACCCATAGACA	900
QY	901	TTTGTGTGCTGAATGATTTACACCAATGGGAAGCATCCCCAACGACAAACCAATTTCAA	960
Db	901	TTTGTGTGCTGTAATGATTTACACCAATGGGAAGCATCCCCAACGACAAACCAATTTCAA	960
QY	961	ATGTGGAACAAGTTTACATATATGGAATAATGCCCAAGTATATCAGGCAAAAACATTTAAAGC	1020
Db	961	ATGTGGAACAAGTTTACATATGGAATAATGCCCAAGTATATCAGGCAAAAACATTTAAAGC	1020
QY	1021	TGGCCACTGGGATGAGGAATATACCGAAAAGCAAAATCAGA	1061
Db	1021	TGGCCACTGGGATGAGGAATGATACCGAAAAGCAAAATCAGA	1061

RESULT 9  
US-10-872-014-7  
; Sequence 7, Application US/10872014

```

H      Publication No. US20040234553A1
H      GENERAL INFORMATION:
H      APPLICANT: The University of Pittsburgh - of the Commonwealth System of
H      APPLICANT: Dowling, Patricia W.
H      APPLICANT: Youngner, Julius S.
H      TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
H      FILE REFERENCE: EQ-1-CI-PUS-1
H      CURRENT APPLICATION NUMBER: US/10/872,014
H      CURRENT FILING DATE: 2004-06-18
H      PRIOR APPLICATION NUMBER: 10/434,811
H      PRIOR FILING DATE: 2003-05-08
H      PRIOR APPLICATION NUMBER: 09/762,861
H      PRIOR FILING DATE: 2001-08-24
H      PRIOR APPLICATION NUMBER: PCT/US99/18583
H      PRIOR FILING DATE: 1999-08-12
H      PRIOR APPLICATION NUMBER: 09/133,921
H      PRIOR FILING DATE: 1998-08-13
H      NUMBER OF SEQ ID NOS: 43
H      SOFTWARE: PatentIn version 3.1
H      SEQ ID NO 7
H      LENGTH: 1762
H      TYPE: DNA
H      ORGANISM: Equine influenza virus H3N8
H      FEATURE:
H      NAME/KEY: CDS
H      LOCATION: (30)..(1724)
H      OTHER INFORMATION:
H      US-10-872-014-7

```

Query Match	97.3%	Score 1032.2	DB 18	Length 1762
Best Local Similarity	98.3%	Pred. No. 3.2e-277	Indels 0	Gaps 0
Matches 1043	Conservative 0	Mismatches 18		
QY	1	AGCAAAAGCAGGGGATATTTCTGTCAAATCATGAAGACAACCATTTATTTTGATACTACTGA	60	
DB	1	AGCAAAAGCAGGGGATATTTCTGTCAAATCATGAAGACAACCATTTATTTTGATACCACTGA	60	
QY	61	CCCATTTGGGTCTACAGTCAAAAACCCACACAGTGGAAACAACACAGGCACACATTTATGTCGG	120	
DB	61	CCCATTTGGGTCTACAGTCAAAAACCCACACAGTGGCAACAACAGGCACACATTTATGTCGG	120	
QY	121	GACACCATGCAGTAGCAAAATGGGAACATTTGGTTAAACAANTAACTGATGACCAAAATTGAGG	180	
DB	121	GACACCATGCAGTAGCAAAATGGGAACATTTGGTTAAACAANTAACTGATGACCAAAATTGAGG	180	
QY	181	TGCAAAATGCTACTGAAATTAGTTTCAGAGCATTTCAATAGGGAATAATGCAACAACATCAT	240	
DB	181	TGCAAAATGCTACTGAAATTAGTTTCAGAGCATTTCAATAGGGAATAATGCAACAACATCAT	240	
QY	241	ATAAAGTTCCTAGATGGGAAGAAATTTGCACTAATATAGATGCATGCTAGGAGACCCCACT	300	
DB	241	ATAAAGTTCCTAGATGGGAAGAAATTTGCACTAATATAGATGCATGCTAGGAGACCCCACT	300	
QY	301	GTGATGTCTTCCAGTATGAGAAATGGGACCTCTTCATAGAAAGAGCAGCGCTTTTCAGCA	360	
DB	301	GTGATGTCTTCCAGTATGAGAAATGGGACCTCTTCATAGAAAGAGCAGCGCTTTTCAGCA	360	
QY	361	ATTGCTACCCATATGACATCCCTGACTATGCAATGCTCCGGTCCGATTTGTAGCATCCTCAG	420	
DB	361	ATTGCTACCCATATGACATCCCTGACTATGCAATGCTCCGGTCCGATTTGTAGCATCCTCAG	420	
QY	421	GAACTATTAGAAATTCACAGCAGAGGGATTCACATGGCAGAGGTGTCACTCAAAAACGGAAGA	480	
DB	421	GAACTATTAGAAATTCACAGCAGAGGGATTCACATGGCAGAGGTGTCACTCAAAAACGGAAGA	480	
QY	481	GTGAGCCTGCAAAAGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTTGGCTTAACAA	540	
DB	481	GTGATCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTTGGCTTAACAG	540	
QY	541	AATCTGGAACCTCTTACCCCACTTGAATGTGCAATGCCTTAAACAATAAAAATTTTCGACA	600	
DB	541	AATCTGGAACCTCTTACCCCACTTGAATGTGCAATGCCTTAAACAATAAAAATTTTCGACA	600	

QY 1021 TGGCCACTGGGATGAGGAATATACAGAAAGCAATCAGA 1061  
|||||  
Db 1021 TGGCCACTGGGATGAGGAATGACAGAAAGCAATCAGA 1061  
|||||

## RESULT 7

US-10-434-811A-7  
; Sequence 7, Application US/10434811A  
; Publication No. US20040022809A1  
; GENERAL INFORMATION:  
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher  
; Education  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C1-PUS-1  
; CURRENT APPLICATION NUMBER: US/10/434,811A  
; CURRENT FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 1762  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (30)..(1724)  
; OTHER INFORMATION:  
US-10-434-811A-7

Query Match 97.3%; Score 1032.2; DB 17; Length 1762;  
Best Local Similarity 98.3%; Pred. No. 3.2e-277;  
Matches 1043; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 AGCAAAAGCAGGGGATTTCTGTCATCATGACGACCAACCATTTTGTACTACTGA 60  
Db 1 AGCAAAAGCAGGGGATTTCTGTCATCATGACGACCAACCATTTTGTACTACTGA 60  
QY 61 CCCATTGGTCTACAGTCAAAACCCCAACCAAGTGGAAACCAACACAGCCACATTTGCTGG 120  
Db 61 CCCATTGGTCTACAGTCAAAACCCCAACCAAGTGGAAACCAACACAGCCACATTTGCTGG 120  
QY 121 GACACCATGCTAGTCAAAATGGAACATTTGGTAAACCAATTAATGATGACCAAAATTTGAGG 180  
Db 121 GACACCATGCTAGTCAAAATGGAACATTTGGTAAACCAATTAATGATGACCAAAATTTGAGG 180  
QY 181 TGACAAATGCTACTGTAATTTAGTTCAGAGCATTTCAATGAGGAAATATGCAACACTCAT 240  
Db 181 TGACAAATGCTACTGTAATTTAGTTCAGAGCATTTCAATGAGGAAATATGCAACACTCAT 240  
QY 241 ATAAGTCTCTAGATGGAAGAAATTTGCACTTAATAGATGCAATGCTAGGAGACCCCACT 300  
Db 241 ATAAGTCTCTAGATGGAAGAAATTTGCACTTAATAGATGCAATGCTAGGAGACCCCACT 300  
QY 301 GTGATGCTTCCAGTATGAGAAATTTGGACCTTTCATAGAAAGAGAGCGGCTTTTCAGCA 360  
Db 301 GTGATGCTTCCAGTATGAGAAATTTGGACCTTTCATAGAAAGAGAGCGGCTTTTCAGCA 360  
QY 361 ATTGCTTACCATATGACATCCCTGACTATGATCGCTCCGCTCCATTTGATGATCCTCAG 420  
Db 361 ATTGCTTACCATATGACATCCCTGACTATGATCGCTCCGCTCCATTTGATGATCCTCAG 420  
QY 421 GAACATTTAGAAATTCACAGCAGAGGGATTCACATGAGCAGGTGCTCACTCAAAACGGAAGAA 480  
Db 421 GAACATTTAGAAATTCACAGCAGAGGGATTCACATGAGCAGGTGCTCACTCAAAACGGAAGAA 480  
QY 481 GTGGAGCTTGCAAAAGGGGATCAGCGGATAGTTTCTTTAGCGGACTGAATTCGGCTTAACAA 540  
|||||

Db 481 GTGGATCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTTGGCTAAACAG 540  
QY 541 AATCTGGAACTCTTACCCCACTTGAATGTCGCAATGCCCTAAACAATAAATTTTCGACA 600  
Db 541 AATCTGGAACTCTTACCCCACTTGAATGTCGCAATGCCCTAAACAATAAATTTTCGACA 600  
QY 601 AACTATACATCTGGGGGATTCATCACCAGGCTCAAAACCAACAGCAGACAGAAATTTGTACA 660  
Db 601 AACTATACATCTGGGGGATTCATCACCAGGCTCAAAACCAACAGCAGACAGAAATTTGTACA 660  
QY 661 TCCAGAAATCAGGACGAGTAACAGTCTCAACAAAAGAAAGTCAACAAACGATAGTCCCTA 720  
Db 661 TCCAGAAATCAGGACGAGTAACAGTCTCAACAAAAGAAAGTCAACAAACGATAGTCCCTA 720  
QY 721 ATATCGGATCTAGACCGGTGGGTAGGGGTCAATCAGGAGGATAGCATATCTGACCA 780  
Db 721 ATATCGGATCTAGACCGGTGGGTAGGGGTCAATCAGGAGGATAGCATATCTGACCA 780  
QY 781 TTGTAAACCTGGAGATATCCTAATGATAAACAAGTAATGGCAACTTAGTTCACCGCGG 840  
Db 781 TTGTAAACCTGGAGATATCCTAATGATAAACAAGTAATGGCAACTTAGTTCACCGCGG 840  
QY 841 GATATTTTAAATTTGAAAACAGGAAAAGCTCTGTAATGAGATCAGATGACCCATAGACA 900  
Db 841 GATATTTTAAATTTGAAAACAGGAAAAGCTCTGTAATGAGATCAGATGACCCATAGACA 900  
QY 901 TTTGTGCTGCTGAATGTATTACCAAAATGAAGCATCCCAACGACAAACCATTTCAAA 960  
Db 901 TTTGTGCTGCTGAATGTATTACCAAAATGAAGCATCCCAACGACAAACCATTTCAAA 960  
QY 961 ATGTGAACAAAGTTACATATGGAATAATGCCCAAGTATATATCAGGCAAAACACTTTAAAGC 1020  
Db 961 ATGTGAACAAAGTTACATATGGAATAATGCCCAAGTATATATCAGGCAAAACACTTTAAAGC 1020  
QY 1021 TGGCCACTGGGATGAGGAATATACAGAAAGCAATCAGA 1061  
Db 1021 TGGCCACTGGGATGAGGAATATACAGAAAGCAATCAGA 1061

## RESULT 8

US-10-734-373-7  
; Sequence 7, Application US/10734373  
; Publication No. US20040137015A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/734,373  
; CURRENT FILING DATE: 2003-12-12  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 1762  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (30)..(1724)  
; OTHER INFORMATION:  
US-10-734-373-7

Query Match 97.3%; Score 1032.2; DB 18; Length 1762;  
Best Local Similarity 98.3%; Pred. No. 3.2e-277;  
Matches 1043; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 AGCAAAAGCAGGGGATTTCTGTCATCATGACGACCAACCATTTTGTACTACTGA 60  
Db 1 AGCAAAAGCAGGGGATTTCTGTCATCATGACGACCAACCATTTTGTACTACTGA 60  
|||||

Db 361 GTTGCTACCATATGACATCCCTGACTATGATCGCTCGGTCCATTTGTAGCATCTCTCAG 420  
Qy 421 GAACATTAGAAATTCACAGCAGAGGAGTTCACATGGACAGGTGTCACTCAAAACGGAGAA 480  
Db 421 GAACATTGGAATTCACAGCAGAGGAGTTCACATGGACAGGTGTCACTCAAAACGGAGAA 480  
Qy 481 GTGGAGCCTGCAAAAGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTTGGCTAACAA 540  
Db 481 GTGGATCCTGCAAAAGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTTGGCTAACAG 540  
Qy 541 AATCTGGAACCTTACCCACATTTGAATGTGCAATGCTTAACAAATAAAATTTTCGACA 600  
Db 541 AATCTGGAACCTTACCCACATTTGAATGTGCAATGCTTAACAAATAAAATTTTCGACA 600  
Qy 601 AACTATACATCTGGGGATTCATACCCGAGTCAAAACCAACAGCAGACAGAAATTTGTACA 660  
Db 601 AACTATACATCTGGGGATTCATACCCGAGTCAAAACCAACAGCAGACAGAAATTTGTACA 660  
Qy 661 TCCAAGAACTCAGACAGAGTAAACAGTCTCAACAAAAAGAGTCAACAAACGATAGTCCCTA 720  
Db 661 TCCAAGAACTCAGACAGAGTAAACAGTCTCAACAAAAAGAGTCAACAAACGATAGTCCCTA 720  
Qy 721 ATATCGGATCTAGACCGTGGTGTAGGGTCAATCAGGCGAGGTAAGCATATATCTGACCA 780  
Db 721 ATATCGGATCTAGACCGTGGTGTAGGGTCAATCAGGCGAGGTAAGCATATATCTGACCA 780  
Qy 781 TTGTAAACCTGAGATATCTTAATGATAACAGTAATGGCACTTAGTTGACACCGCGG 840  
Db 781 TTGTAAACCTGAGATATCTTAATGATAACAGTAATGGCACTTAGTTGACACCGCGG 840  
Qy 841 GATATTTAAATTTGAAAAACAGGAAAGCTCTCTAATGAGATCAGATGCAACCCATAGACA 900  
Db 841 GATATTTAAATTTGAAAAACAGGAAAGCTCTCTAATGAGATCAGATGCAACCCATAGACA 900  
Qy 901 TTGTGTGTGAATGTATTTACACCAATGGAAGCATCCCAACGACAAACCAATTTCAA 960  
Db 901 TTGTGTGTGTGAATGTATTTACACCAATGGAAGCATCCCAACGACAAACCAATTTCAA 960  
Qy 961 ATGTGAACAAGTTACATATGGAATGCCCCAAGTATATATCAGGCAAAACACATTTAAAGC 1020  
Db 961 ATGTGAACAAGTTACATATGGAATGCCCCAAGTATATATCAGGCAAAACACATTTAAAGC 1020

RESULT 6

US-10-065-133A-7  
; Sequence 7, Application US/10065133A  
; Publication No. US20030199074A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/065,133A  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 1762  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (30)..(1724)  
; OTHER INFORMATION:

US-10-065-133A-7  
Query Match 97.3%; Score 1032.2; DB 16; Length 1762;  
Best Local Similarity 98.3%; Pred. No. 3.2e-277;  
Matches 1043; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
Qy 1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAAACCAATTTTGTACTACTGA 60  
Db 1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAAACCAATTTTGTACTACTGA 60  
Qy 61 CCCATTGGGTCTACAGTCAAAACCCAAACAGTGGGAAAACACACAGCACAATTTGTCTGG 120  
Db 61 CCCATTGGGTCTACAGTCAAAACCCAAACAGTGGGAAAACACACAGCACAATTTGTCTGG 120  
Qy 121 GACACATGCTAGTCAATGGAACATTTGGTAAAAACAATACTGATGACCAAAATTTGAGG 180  
Db 121 GACACATGCTAGTCAATGGAACATTTGGTAAAAACAATACTGATGACCAAAATTTGAGG 180  
Qy 181 TGACAAATGCTACTGAATTTAGTTTCAGAGCATTTCAATAGGGAAAATATGCAACAACTCAT 240  
Db 181 TGACAAATGCTACTGAATTTAGTTTCAGAGCATTTCAATAGGGAAAATATGCAACAACTCAT 240  
Qy 241 ATAAAGTTCTAGATGGAAGAAATTTGCACATTAATAGATGCAATGCTAGGAGACCCCACT 300  
Db 241 ATAAAGTTCTAGATGGAAGAAATTTGCACATTAATAGATGCAATGCTAGGAGACCCCACT 300  
Qy 301 GTGATGTCTTCCAGTATGAGAAATTTGGGACCTCTTCATAGAAAAGAGCAGCGCTTTTCAGCA 360  
Db 301 GTGATGTCTTCCAGTATGAGAAATTTGGGACCTCTTCATAGAAAAGAGCAGCGCTTTTCAGCA 360  
Qy 361 ATTGTGATCCCATATGACATTCCTGATATGCTATGCTCGGTCCATTTGTAGCATCTCTCAG 420  
Db 361 ATTGTGATCCCATATGACATTCCTGATATGCTATGCTCGGTCCATTTGTAGCATCTCTCAG 420  
Qy 421 GAACATTAGAAATTTACAGCAGAGGAGTTCACATGACAGCGTGTCACTCAAAACGGAGAA 480  
Db 421 GAACATTAGAAATTTACAGCAGAGGAGTTCACATGACAGCGTGTCACTCAAAACGGAGAA 480  
Qy 481 GTGGAGCCTGCAAAAGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTTGGCTAACAA 540  
Db 481 GTGGAGCCTGCAAAAGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTTGGCTAACAG 540  
Qy 541 AATCTGGAACCTTCTACCCCAATTTGAATGTGCAATGCTTAACAAATAAAATTTTCGACA 600  
Db 541 AATCTGGAACCTTCTACCCCAATTTGAATGTGCAATGCTTAACAAATAAAATTTTCGACA 600  
Qy 601 AACTATACATCTGGGGATTCATACCCGAGTCAAAACCAACAGCAGACAGAAATTTGTACA 660  
Db 601 AACTATACATCTGGGGATTCATACCCGAGTCAAAACCAACAGCAGACAGAAATTTGTACA 660  
Qy 661 TCCAAGAACTCAGACAGAGTAAACAGTCTCAACAAAAAGAGTCAACAAACGATAGTCCCTA 720  
Db 661 TCCAAGAACTCAGACAGAGTAAACAGTCTCAACAAAAAGAGTCAACAAACGATAGTCCCTA 720  
Qy 721 ATATCGGATCTAGACCGTGGTGTAGGGTCAATCAGGCGAGGTAAGCATATATCTGACCA 780  
Db 721 ATATCGGATCTAGACCGTGGTGTAGGGTCAATCAGGCGAGGTAAGCATATATCTGACCA 780  
Qy 781 TTGTAAACCTGAGATATCTTAATGATAACAGTAATGGCACTTAGTTGACACCGCGG 840  
Db 781 TTGTAAACCTGAGATATCTTAATGATAACAGTAATGGCACTTAGTTGACACCGCGG 840  
Qy 841 GATATTTAAATTTGAAAAACAGGAAAGCTCTGTAAATGAGATCAGATGCAACCCATAGACA 900  
Db 841 GATATTTAAATTTGAAAAACAGGAAAGCTCTGTAAATGAGATCAGATGCAACCCATAGACA 900  
Qy 901 TTGTGTGTGAATGTATTTACACCAATGGAAGCATCCCAACGACAAACCAATTTCAA 960  
Db 901 TTGTGTGTGAATGTATTTACACCAATGGAAGCATCCCAACGACAAACCAATTTCAA 960  
Qy 961 ATGTGAACAAGTTACATATGGAATGCCCCAAGTATATATCAGGCAAAACACATTTAAAGC 1020  
Db 961 ATGTGAACAAGTTACATATGGAATGCCCCAAGTATATATCAGGCAAAACACATTTAAAGC 1020

TYPE: DNA  
ORGANISM: Equine influenza virus H3N8  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (30)..(1724)  
OTHER INFORMATION:  
US-10-734-373-10

Query Match 97.4%; Score 1033.8; DB 18; Length 1762;  
Best Local Similarity 98.4%; Pred. No. 1.1e-277; Mismatches 0; Gaps 0;  
Matches 1044; Conservative 0; Indels 17; Indels 0; Gaps 0;

QY 1 AGCAAAAGCAGGGGATATTTCTGTCATCATGAAGACACCACTATTTTGTATCTACTGA 60  
Db 1 AGCAAAAGCAGGGGATATTTCTGTCATCATGAAGACACCACTATTTTGTATCTACTGA 60  
QY 61 CCATTGGTCTACAGTCAAAACCCACAGTGGGAAACACACAGCCACATTTATGTCGG 120  
Db 61 CCATTGGTCTACAGTCAAAACCCACAGTGGGAAACACACAGCCACATTTATGTCGG 120  
QY 121 GACACCATGCTAGCAATGAACATTTGGTAAACCAATACTGATGACCAAAATTTGAGG 180  
Db 121 GACACCATGCTAGCAATGAACATTTGGTAAACCAATACTGATGACCAAAATTTGAGG 180  
QY 181 TGACAAATGCTACTGAAATTTAGTTCAGAGCAATTTCAATAGGGAATAATGCAAACTCAT 240  
Db 181 TGACAAATGCTACTGAAATTTAGTTCAGAGCAATTTCAATAGGGAATAATGCAAACTCAT 240  
QY 241 ATAAAGTTCTAGATGAAGAAATTTGCACATTAATAGATGCAATGCTAGGAGACCCCACT 300  
Db 241 ATAAAGTTCTAGATGAAGAAATTTGCACATTAATAGATGCAATGCTAGGAGACCCCACT 300  
QY 241 ATAGAGTTCTAGATGAAGAAATTTGCACATTAATAGATGCAATGCTAGGAGACCCCACT 300  
Db 241 ATAGAGTTCTAGATGAAGAAATTTGCACATTAATAGATGCAATGCTAGGAGACCCCACT 300  
QY 301 GTGATGCTCTCCAGTATGAAATTTGGACCTCTTATGAAAGAGAGCGCTTTTCAGCA 360  
Db 301 GTGATGCTCTCCAGTATGAAATTTGGACCTCTTATGAAAGAGAGCGCTTTTCAGCA 360  
QY 361 ATTGCTACCCATATGACATCCCTGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
Db 361 ATTGCTACCCATATGACATCCCTGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
QY 421 GAACATTTAGAAATTCAGCAGAGAGGATTCACATGAGCAGGTGTCTACTCAAAACGGAAGA 480  
Db 421 GAACATTTAGAAATTCAGCAGAGAGGATTCACATGAGCAGGTGTCTACTCAAAACGGAAGA 480  
QY 481 GTGAGCTCTGCAAAAGGAGATCAGCGGATGTTCTTTAGCGGCTGAAATTTGGCTAACAG 540  
Db 481 GTGAGCTCTGCAAAAGGAGATCAGCGGATGTTCTTTAGCGGCTGAAATTTGGCTAACAG 540  
QY 541 AATCTGGAACCTTTACCCCAATTTGAATGTGACATGCTTAAACAAATTTTCGACA 600  
Db 541 AATCTGGAACCTTTACCCCAATTTGAATGTGACATGCTTAAACAAATTTTCGACA 600  
QY 601 AACTATACATCTGGGGATTCATCCCGAGCTCAAAACCAACAGCGAGACAGATTTGTACA 660  
Db 601 AACTATACATCTGGGGATTCATCCCGAGCTCAAAACCAACAGCGAGACAGATTTGTACA 660  
QY 661 TCCAGAAATCAGCAGGATTAACAGTCTCAACAAAGAGAGTCAACAAAGATGATGCTTCTA 720  
Db 661 TCCAGAAATCAGCAGGATTAACAGTCTCAACAAAGAGAGTCAACAAAGATGATGCTTCTA 720  
QY 721 ATATCGGATCTAGACCGTGGGTTAGGGGTCAATTCAGGCGAGGATTAAGCATATCTGACCA 780  
Db 721 ATATCGGATCTAGACCGTGGGTTAGGGGTCAATTCAGGCGAGGATTAAGCATATCTGACCA 780  
QY 781 TTGTAAACCTGAGATATCTTAATGATAACAGTAAATGGCACTTAGTTGACCGCGGG 840  
Db 781 TTGTAAACCTGAGATATCTTAATGATAACAGTAAATGGCACTTAGTTGACCGCGGG 840  
QY 841 GATATTTTAAATTTGAAACAGGGAAGGCTCTGTATGATGATGATGATGATGATGATGATG 900  
Db 841 GATATTTTAAATTTGAAACAGGGAAGGCTCTGTATGATGATGATGATGATGATGATGATG 900  
QY 901 TTTGTGTCGTGAATGTATTATACCAAAATGGAAGCATCCCAACGACCAAAACCAATTTCAA 960

Db 901 TTTGTGTCGTGAATGTATTATACCAAAATGGAAGCATCCCAACGACAAACCAATTTCAA 960  
QY 961 ATGTGAACAAATTTACATATGGAATGCCCCCAAGTATATCAGGCAAAACCACTTTAAGC 1020  
Db 961 ATGTGAACAAATTTACATATGGAATGCCCCCAAGTATATCAGGCAAAACCACTTTAAGC 1020  
QY 1021 TGGCCACTGGGATGAGGAATATACCAAAAGCAAAATCAGA 1061  
Db 1021 TGGCCACTGGGATGAGGAATATACCAAAAGCAAAATCAGA 1061

RESULT 5

US-10-872-014-10  
Sequence 10, Application US/10872014  
Publication No. US20040234553A1  
GENERAL INFORMATION:  
APPLICANT: The University of Pittsburgh - of the Commonwealth System of  
APPLICANT: Dowling, Patricia W.  
APPLICANT: Youngner, Julius S.  
TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
FILE REFERENCE: EQ-1-CI-PUS-1  
CURRENT APPLICATION NUMBER: US/10/872,014  
CURRENT FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 10/434,811  
PRIOR FILING DATE: 2003-05-08  
PRIOR APPLICATION NUMBER: 09/762,861  
PRIOR FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: PCT/US99/18583  
PRIOR FILING DATE: 1999-08-12  
PRIOR APPLICATION NUMBER: 09/133,921  
PRIOR FILING DATE: 1998-08-13  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 10  
LENGTH: 1762  
TYPE: DNA  
ORGANISM: Equine influenza virus H3N8  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (30)..(1724)  
OTHER INFORMATION:  
US-10-872-014-10

Query Match 97.4%; Score 1033.8; DB 18; Length 1762;  
Best Local Similarity 98.4%; Pred. No. 1.1e-277; Mismatches 0; Gaps 0;  
Matches 1044; Conservative 0; Indels 17; Indels 0; Gaps 0;

QY 1 AGCAAAAGCAGGGGATATTTCTGTCATCATGAAGACACCACTATTTTGTATCTACTGA 60  
Db 1 AGCAAAAGCAGGGGATATTTCTGTCATCATGAAGACACCACTATTTTGTATCTACTGA 60  
QY 61 CCATTGGTCTACAGTCAAAACCCACAGTGGGAAACACACAGCCACATTTATGTCGG 120  
Db 61 CCATTGGTCTACAGTCAAAACCCACAGTGGGAAACACACAGCCACATTTATGTCGG 120  
QY 121 GACACCATGCTAGCAATGAACATTTGGTAAACCAATACTGATGACCAAAATTTGAGG 180  
Db 121 GACACCATGCTAGCAATGAACATTTGGTAAACCAATACTGATGACCAAAATTTGAGG 180  
QY 181 TGACAAATGCTACTGAAATTTAGTTCAGAGCAATTTCAATAGGGAATAATGCAAACTCAT 240  
Db 181 TGACAAATGCTACTGAAATTTAGTTCAGAGCAATTTCAATAGGGAATAATGCAAACTCAT 240  
QY 241 ATAAAGTTCTAGATGAAGAAATTTGCACATTAATAGATGCAATGCTAGGAGACCCCACT 300  
Db 241 ATAAAGTTCTAGATGAAGAAATTTGCACATTAATAGATGCAATGCTAGGAGACCCCACT 300  
QY 301 GTGATGCTCTCCAGTATGAGAAATTTGGGACCTCTTATGAAAGAGAGCGCTTTTCAGCA 360  
Db 301 GTGATGCTCTCCAGTATGAGAAATTTGGGACCTCTTATGAAAGAGAGCGCTTTTCAGCA 360  
QY 361 ATTGCTACCCATATGACATCCCTGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

```
QY 781 TTGTAAACCTGGAGATATCTTAATGATAAAGCAGTAATGCGCACTTAGTTGACCGCGG 840
DB 781 TTGTAAACCTGGAGATATCTTAATGATAAAGCAGTAATGCGCACTTAGTTGACCGCGG 840
QY 841 GATATTTTAAATTTGAAACACAGGGAAGCTCTGTAATGAGATCAGATGCAACCATAGACA 900
DB 841 GATATTTTAAATTTGAAACACAGGGAAGCTCTGTAATGAGATCAGATGCAACCATAGACA 900
QY 901 TTGTGTCTGCTGAATGATATACCAAAATGGAAGCATCCCAACGACCAACCATTTCAA 960
DB 901 TTGTGTCTGCTGAATGATATACCAAAATGGAAGCATCCCAACGACCAACCATTTCAA 960
QY 961 ATGTGAACAAAGTTACATATGGAATGCGCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
DB 961 ATGTGAACAAAGTTACATATGGAATGCGCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
QY 1021 TGCCCACTGGGATGAGGAATATACCAAGAAAGCAATCAGA 1061
DB 1021 TGCCCACTGGGATGAGGAATATACCAAGAAAGCAATCAGA 1061

RESULT 3
US-10-434-811A-10
; Sequence 10, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; Education
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-CL-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (30)..(1724)
; OTHER INFORMATION:
US-10-434-811A-10

Query Match 97.4%; Score 1033.8; DB 17; Length 1762;
Best Local Similarity 98.4%; Pred. No. 1.1e-277; Indels 0; Gaps 0;
Matches 1044; Conservative 0; Mismatches 17;

QY 1 AGCAAAAGCAGGGGATATTTCTGTCATCATGATGAAGCAACCATATTTTGATACTACTGA 60
DB 1 AGCAAAAGCAGGGGATATTTCTGTCATCATGATGAAGCAACCATATTTTGATACTACTGA 60
QY 61 CCATTTGGGTCTACAGTCAAAACCCCAACAGTGGAAACACACAGCCACATTTGCTGG 120
DB 61 CCATTTGGGTCTACAGTCAAAACCCCAACAGTGGCAACACACAGCCACATTTGCTGG 120
QY 121 GACACCATGAGTAGCAAAATGGAACATTTGTTGTAACCAATTAATGATGACCAATTTGAGG 180
DB 121 GACACCATGAGTAGCAAAATGGAACATTTGTTGTAACCAATTAATGATGACCAATTTGAGG 180
QY 181 TGACAAATGCTACTGAATTTAGTTCAGAGCATTTCAATAGGAAATATGCAACCACTCAT 240
DB 181 TGACAAATGCTACTGAATTTAGTTCAGAGCATTTCAATAGGAAATATGCAACCACTCAT 240
QY 241 ATAAAGTCTAGATGGAAGAAATTTGCAATTAATGATGCAATGCAATGAGGAGACCCCACT 300
DB 241 ATAGAGTTCTAGATGGAAGAAATTTGCAATTAATGATGCAATGCAATGAGGAGACCCCACT 300
```

```
QY 301 GTGATGCTCTCCAGTATGAGAAATTTGGACCTCTTTCATAGAAAGACGACGCTTTTCAGCA 360
DB 301 GTGATGCTCTTTCAGTATGAGAAATTTGGACCTCTTTCATAGAAAGACGACGCTTTTCAGCA 360
QY 361 ATTGCTACCCATATGACATCCCTGACTATGATCGCTCCGCTCCGTTCCATTTAGCATCCTCAG 420
DB 361 GTTGTACCCCATATGACATCCCTGACTATGATCGCTCCGCTCCGTTCCATTTAGCATCCTCAG 420
QY 421 GAACATTTAGAAATTTACAGCAGAGGGATTCACATGGACAGAGGTGTCACTCAAAACGGAAGA 480
DB 421 GAACATTTAGAAATTTACAGCAGAGGGATTCACATGGACAGAGGTGTCACTCAAAACGGAAGA 480
QY 481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTTGGCTTAACAA 540
DB 481 GTGGATCTCTGAAAGGGAATCAGCCGATAGTTTCTTTAGCCGACTGAATTTGGCTTAACAG 540
QY 541 AATCTGGAAACTCTTTACCCCACTTTGAATGTGACAAATGCCTTAACAATAATTTTCGACA 600
DB 541 AATCTGGAAACTCTTTACCCCACTTTGAATGTGACAAATGCCTTAACAATAATTTTCGACA 600
QY 601 AACTATACATCTGGGGGATTCATCACCCGAGCTCAAAACCAACAGCAGACAGAAATTTGTACA 660
DB 601 AACTATACATCTGGGGGATTCATCACCCGAGCTCAAAACCAACAGCAGACAGAAATTTGTACA 660
QY 661 TCCAAAGAAATCAGGACGAGTAAACAGTCTTCAACAAAGAAAGTCAACAAACGATAGTCCCTA 720
DB 661 TCCAAAGAAATCAGGACGAGTAAACAGTCTTCAACAAAGAAAGTCAACAAACGATAGTCCCTA 720
QY 721 ATATCGATCTAGACCGTGGGTAGGGTCAATCAGGAGGATAGCATATATCTGACCA 780
DB 721 ACATCGATCTAGACCGTGGGTAGGGTCAATCAGGAGGATAGCATATATCTGACCA 780
QY 781 TTGTAAACCTGGAGATATCTTAATGATAAAGCAGTAATGCGCACTTAGTTGACCGCGGG 840
DB 781 TTGTAAACCTGGAGATATCTTAATGATAAAGCAGTAATGCGCACTTAGTTGACCGCGGG 840
QY 841 GATATTTTAAATTTGAAACACAGGGAAGCTCTGTAATGAGATCAGATGCAACCATAGACA 900
DB 841 GATATTTTAAATTTGAAACACAGGGAAGCTCTGTAATGAGATCAGATGCAACCATAGACA 900
QY 901 TTGTGTCTGCTGAATGATATACCAAAATGGAAGCATCCCAACGACCAACCATTTCAA 960
DB 901 TTGTGTCTGCTGAATGATATACCAAAATGGAAGCATCCCAACGACCAACCATTTCAA 960
QY 961 ATGTGAACAAAGTTACATATGGAATGCGCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
DB 961 ATGTGAACAAAGTTACATATGGAATGCGCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
QY 1021 TGCCCACTGGGATGAGGAATATACCAAGAAAGCAATCAGA 1061
DB 1021 TGCCCACTGGGATGAGGAATATACCAAGAAAGCAATCAGA 1061
```

```
RESULT 4
US-10-734-373-10
; Sequence 10, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/734,373
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1762
```

```
Db 121 GACACCATGCTAGCAATGGAATGCAATTTGGTAAAAACAATAACTGATGACCAAAATTGAGG 180
Qy 181 TCACAAATGCTACTGAAATTTAGTTTCAGACATTTCAATAGGGAATAATGCAACAACTCAT 240
Db 181 TCACAAATGCTACTGAAATTTAGTTTCAGACATTTCAATAGGGAATAATGCAACAACTCAT 240
Qy 241 ATAAAGTTCTTAGATGGAAGAAATTTGCACATTAATAGATGCAATGCTAGGAGACCCCACT 300
Db 241 ATAAAGTTCTTAGATGGAAGAAATTTGCACATTAATAGATGCAATGCTAGGAGACCCCACT 300
Qy 301 GTGATGCTTCCAGTATGAGAAATTTGGACCTTTCATAGAAAGAGCAGCGCTTTCAGCA 360
Db 301 GTGATGCTTCCAGTATGAGAAATTTGGACCTTTCATAGAAAGAGCAGCGCTTTCAGCA 360
Qy 361 ATTGCTTACCCTATGACATCCCTGACTATGCAATGCTCCGGTCCATTTGATGATCCTCAG 420
Db 361 ATTGCTTACCCTATGACATCCCTGACTATGCAATGCTCCGGTCCATTTGATGATCCTCAG 420
Qy 421 GAACATTTAGAAATTTACAGCAGAGGGATTTCAATGAGCAGGTGTCACTCAAAAACGGAAGAA 480
Db 421 GAACATTTAGAAATTTACAGCAGAGGGATTTCAATGAGCAGGTGTCACTCAAAAACGGAAGAA 480
Qy 481 GTGAGCCTGCAAAAGGGGATCAGCGGATAGTTTCTTTAGCCGACTGAATTTGGCTAAACAA 540
Db 481 GTGAGCCTGCAAAAGGGGATCAGCGGATAGTTTCTTTAGCCGACTGAATTTGGCTAAACAA 540
Qy 541 AATCTGGAATCTTACCCCAATGAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 600
Db 541 AATCTGGAATCTTACCCCAATGAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 600
Qy 601 AACTATACATCTGGGGATTTCACTACCCGAGTCTCAACCAACAGCAGACAGAAATTTGTACA 660
Db 601 AACTATACATCTGGGGATTTCACTACCCGAGTCTCAACCAACAGCAGACAGAAATTTGTACA 660
Qy 661 TCCAGAAATCAGAACGAGTAAAGTCTCAACCAAAAGAAAGTCAACCAAGATGATGCTCCCTA 720
Db 661 TCCAGAAATCAGAACGAGTAAAGTCTCAACCAAAAGAAAGTCAACCAAGATGATGCTCCCTA 720
Qy 721 ATATCGGATCTAGACCGTGGGTTAGGGTCAATCAGGAGGATAGCATATATCTGACCA 780
Db 721 ATATCGGATCTAGACCGTGGGTTAGGGTCAATCAGGAGGATAGCATATATCTGACCA 780
Qy 781 TTGTAAACCTGGAGATCTTAATGATAAAGTAAATGCAATGCAATGCAATGCAATGCAATGCA 840
Db 781 TTGTAAACCTGGAGATCTTAATGATAAAGTAAATGCAATGCAATGCAATGCAATGCAATGCA 840
Qy 841 GATATTTAAATTTGAAACAGGAAAGTCTGTAATGAGATCAGATGACCCCATAGACA 900
Db 841 GATATTTAAATTTGAAACAGGAAAGTCTGTAATGAGATCAGATGACCCCATAGACA 900
Qy 901 TTGTGTGCTGATGTAATTTACACCAATGGAAGCATCCCAACGACCAACCAATTTCAA 960
Db 901 TTGTGTGCTGATGTAATTTACACCAATGGAAGCATCCCAACGACCAACCAATTTCAA 960
Qy 961 ATGTGAAACAAAGTTACATATGAAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
Db 961 ATGTGAAACAAAGTTACATATGAAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
Qy 1021 TGGCCACTGGGATGAGGAATATACGAGAAAGCAATCAGA 1061
Db 1021 TGGCCACTGGGATGAGGAATATATACGAGAAAGCAATCAGA 1061
```

## RESULT 2

```
US-10-065-133A-10
; Sequence 10, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Fournier, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
```

```
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (30)..(1724)
; OTHER INFORMATION:
US-10-065-133A-10
```

```
Query Match 97.4%; Score 1033.8; DB 16; Length 1762;
Best Local Similarity 98.4%; Pred. No. 1.1e-277;
Matches 1044; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
```

```
Qy 1 AGCAAAACGAGGGATATTTCTGTCATCATCAAGACAAACCATTTATTTTGATACTACTGA 60
Db 1 AGCAAAACGAGGGATATTTCTGTCATCATCAAGACAAACCATTTATTTTGATACTACTGA 60
Qy 61 CCCATTGGGTCTACAGTCAAAACCCCAACGAGTGGAAACAAACACAGCCACATTTATGCTGG 120
Db 61 CCCATTGGGTCTACAGTCAAAACCCCAACGAGTGGAAACAAACACAGCCACATTTATGCTGG 120
Qy 121 GACACCATGCAAGTACCAATGGAACATTTGGTAAACAAATAACTGATGACCAAAATGAGG 180
Db 121 GACACCATGCAAGTACCAATGGAACATTTGGTAAACAAATAACTGATGACCAAAATGAGG 180
Qy 181 TGACAAATGCTACTGAAATTTAGTTCAGACATTTCAATAGGGAATAATATGCAACACTCAT 240
Db 181 TGACAAATGCTACTGAAATTTAGTTCAGACATTTCAATAGGGAATAATATGCAACACTCAT 240
Qy 241 ATAAAGTTCTAGATGGAAGAAATTTGCACATTAATAGATGCAATGCTAGGAGACCCCACT 300
Db 241 ATAGAGTTCTAGATGGAAGAAATTTGCACATTAATAGATGCAATGCTAGGAGACCCCACT 300
Qy 301 GTGATGCTTCCAGTATGAGAAATTTGGGACCTTTCATAGAAAGAGCAGCGCTTTCAGCA 360
Db 301 GTGATGCTTCCAGTATGAGAAATTTGGGACCTTTCATAGAAAGAGCAGCGCTTTCAGCA 360
Qy 361 ATTGCTTACCCTATGACATCCCTGACTATGCAATGCTCCGGTCCATTTGATGATCCTCAG 420
Db 361 ATTGCTTACCCTATGACATCCCTGACTATGCAATGCTCCGGTCCATTTGATGATCCTCAG 420
Qy 421 GAACTATGAAATTTACAGCAGAGGGATTTCAATGAGCAGGTGTCACTCAAAAACGGAAGAA 480
Db 421 GAACTATGAAATTTACAGCAGAGGGATTTCAATGAGCAGGTGTCACTCAAAAACGGAAGAA 480
Qy 481 GTGAGCCTGCAAAAGGGGATCAGCGGATAGTTTCTTTAGCCGACTGAATTTGGCTAAACAA 540
Db 481 GTGAGCCTGCAAAAGGGGATCAGCGGATAGTTTCTTTAGCCGACTGAATTTGGCTAAACAA 540
Qy 541 AATCTGGAATCTTACCCCAATGAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 600
Db 541 AATCTGGAATCTTACCCCAATGAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 600
Qy 601 AACTATACATCTGGGGATTTCACTACCCGAGTCTCAACCAACAGCAGACAGAAATTTGTACA 660
Db 601 AACTATACATCTGGGGATTTCACTACCCGAGTCTCAACCAACAGCAGACAGAAATTTGTACA 660
Qy 661 TCCAGAAATCAGAACGAGTAAAGTCTCAACCAAAAGAAAGTCAACCAAGATGATGCTCCCTA 720
Db 661 TCCAGAAATCAGAACGAGTAAAGTCTCAACCAAAAGAAAGTCAACCAAGATGATGCTCCCTA 720
Qy 721 ATATCGGATCTAGACCGTGGGTTAGGGTCAATCAGGAGGATAGCATATATCTGACCA 780
Db 721 ATATCGGATCTAGACCGTGGGTTAGGGTCAATCAGGAGGATAGCATATATCTGACCA 780
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 05:06:27 ; Search time 2061 Seconds  
(without alignments)  
3050.419 Million cell updates/sec

Title: US-10-826-929A-1  
Perfect score: 1061  
Sequence: 1 agcaaaagcaggggatattt.....taccagaaaagcaaatcaga 1061

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5394803 seqs, 2962729879 residues  
Total number of hits satisfying chosen parameters: 10789606

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
19: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1061	100.0	1061	19	US-10-826-929A-1
2	1033.8	97.4	1762	16	US-10-065-133A-10
3	1033.8	97.4	1762	17	US-10-434-811A-10
4	1033.8	97.4	1762	18	US-10-734-373-10
5	1033.8	97.4	1762	18	US-10-872-014-10
6	1032.2	97.3	1762	16	US-10-065-133A-7
7	1032.2	97.3	1762	17	US-10-434-811A-7
8	1032.2	97.3	1762	18	US-10-734-373-7
9	1032.2	97.3	1762	18	US-10-872-014-7
10	1004.8	94.7	1695	16	US-10-065-133A-12
11	1004.8	94.7	1695	17	US-10-434-811A-12

12	1004.8	94.7	1695	18	US-10-734-373-12	Sequence 12, Appl
13	1004.8	94.7	1695	18	US-10-872-014-12	Sequence 12, Appl
14	1003.2	94.6	1695	16	US-10-065-133A-9	Sequence 9, Appl
15	1003.2	94.6	1695	17	US-10-434-811A-9	Sequence 9, Appl
16	1003.2	94.6	1695	18	US-10-734-373-9	Sequence 9, Appl
17	1003.2	94.6	1695	18	US-10-872-014-9	Sequence 9, Appl
18	1003.2	94.6	1695	18	US-10-872-014-9	Sequence 9, Appl
19	125.2	11.8	1711	13	US-10-099-619-1	Sequence 1, Appl
20	124.2	11.7	1775	18	US-10-855-875-7	Sequence 7, Appl
21	123.6	11.6	1733	17	US-10-397-635-13	Sequence 13, Appl
22	122.4	11.5	1110	9	US-09-918-568-57	Sequence 57, Appl
23	105.4	9.9	1754	9	US-09-918-568-27	Sequence 27, Appl
24	98.2	9.3	1728	9	US-09-918-568-28	Sequence 28, Appl
25	96.6	9.1	1783	9	US-09-918-568-46	Sequence 46, Appl
26	94.8	8.9	1683	19	US-10-617-569-2	Sequence 2, Appl
27	92.8	8.7	1847	18	US-10-839-509-3	Sequence 3, Appl
28	91.8	8.7	1773	18	US-10-381-530-4	Sequence 37, Appl
29	79	7.4	329	9	US-09-918-568-37	Sequence 37, Appl
30	77.4	7.3	334	9	US-09-918-568-38	Sequence 38, Appl
31	75.8	7.1	329	9	US-09-918-568-39	Sequence 39, Appl
32	74.8	7.0	329	9	US-09-918-568-41	Sequence 41, Appl
33	72.6	6.8	334	9	US-09-918-568-40	Sequence 40, Appl
34	48.8	4.6	1135	9	US-09-918-568-49	Sequence 49, Appl
35	48.6	4.6	424	9	US-09-918-568-31	Sequence 31, Appl
36	48.6	4.6	429	9	US-09-918-568-32	Sequence 32, Appl
37	47	4.4	424	9	US-09-918-568-30	Sequence 30, Appl
38	43.4	4.1	1691139	14	US-10-067-514-1	Sequence 1, Appl
39	43.4	4.1	1691139	17	US-10-419-723-1	Sequence 1, Appl
40	40.8	3.8	116792	13	US-10-087-192-1090	Sequence 1090, Ap
41	40.6	3.8	442	9	US-09-918-568-29	Sequence 29, Appl
42	40.2	3.8	8866	14	US-10-239-676-140	Sequence 140, App
43	40.2	3.8	8866	15	US-10-240-453-154	Sequence 154, App
44	38.6	3.6	81748	13	US-10-087-192-364	Sequence 364, App
45	38.6	3.6	253861	18	US-10-741-601-5611	Sequence 5611, Ap

ALIGNMENTS

RESULT 1  
US-10-826-929A-1  
; Sequence 1, Application US/10826929A  
; Publication No. US20050032732A1  
; GENERAL INFORMATION:  
; APPLICANT: Lai, Alexander  
; TITLE OF INVENTION: DNA Vaccine Expressing HAI of Equine-2 Influenza Virus  
; FILE REFERENCE: 57657/04-265  
; CURRENT APPLICATION NUMBER: US/10/826,929A  
; CURRENT FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: US 60/470,843  
; PRIOR FILING DATE: 2003-05-15  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 1  
; LENGTH: 1061  
; TYPE: DNA  
; ORGANISM: A/Eq/Kentucky/98  
US-10-826-929A-1

Query Match	100.0%;	Score 1061;	DB 19;	Length 1061;
Best Local Similarity	100.0%;	Pred. No. 2.2e-285;		
Matches 1061;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	AGCAAAAGCAGGGGATATTTCGTCAATCATGAGCAACCACTATTATTTGATCTACTGA	60	
DB	1	AGCAAAAGCAGGGGATATTTCGTCAATCATGAGCAACCACTATTATTTGATCTACTGA	60	
QY	61	CCCATTTGGTCTACAGTCAAAACCCCAACCAAGTGGAAACACACAGCCACATTATGCTCTGG	120	
DB	61	CCCATTTGGTCTACAGTCAAAACCCCAACCAAGTGGAAACACACAGCCACATTATGCTCTGG	120	
QY	121	GAACCAATCAGTAGCAAAATGGAAACATTGGTGTGTAATAAATAATGATGACCAATTTGAGG	180	

Db 1021 AAGCAAAATCAGA 1032

RESULT 15

US-10-065-133A-12  
; Sequence 12, Application US/10065133A  
; Patent No. 6685946  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/065,133A  
; PRIOR FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 1695  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
US-10-065-133A-12

Query Match 94.7%; Score 1004.8; DB 4; Length 1695;  
Best Local Similarity 98.4%; Pred. No. 2.2e-294;  
Matches 1015; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 30 ATGAAGACAAACCAATTATTTGATATCTACTGACCCATTGGGTCTACAGTCACAAACCAACC 89  
Db 1 ATGAAGACAAACCAATTATTTGATATCTACTGACCCATTGGGTCTACAGTCACAAACCAACC 60  
QY 90 AGTGGAAACAAACACAGCCCACTATTGTCTGGGACACCAATGCGAGTAGCAAAATGGAAACATTG 149  
Db 61 AGTGGCAACAAACACAGCCCACTATTGTCTGGGACACCAATGCGAGTAGCAAAATGGAAACATTG 120  
QY 150 GTAAAGCAAAATACCTGATGACCAAAATGGAGGTGACAAATGCTACTGMAATTAGTTTCAGAGC 209  
Db 121 GTAAAGCAAAATACCTGATGACCAAAATGGAGGTGACAAATGCTACTGMAATTAGTTTCAGAGC 180  
QY 210 ATTTCAATAGGAAATATGCAACAACTCATATATAAGTTCTAGATGGAAGAAATTCACAC 269  
Db 181 ATTTCAATAGGAAATATGCAACAACTCATATAGTTCTAGATGGAAGAAATTCACAC 240  
QY 270 TTAATAGATGCAATGCTAGGAGACCCCACTGTGTATGTTCTTCCAGTATGAGAAATGGGAC 329  
Db 241 TTAATAGATGCAATGCTAGGAGACCCCACTGTGTATGTTCTTCCAGTATGAGAAATGGGAC 300  
QY 330 CTCTTCATAGAAGAGCAGCGCTTTTACGCAATTTGCTACCCATATGACATCCCTGACTAT 389  
Db 301 CTCTTCATAGAAGAGCAGCGCTTTTACGCAATTTGCTACCCATATGACATCCCTGACTAT 360  
QY 390 GCATCGCTCCGCTCCATTGTAGCATCCTCAGAAACATTAGAATTCACAGCAGAGGGATTTC 449  
Db 361 GCATCGCTCCGCTCCATTGTAGCATCCTCAGAAACATTAGAATTCACAGCAGAGGGATTTC 420  
QY 450 ACATGGACAGAGGTGTCTCAAAACGGAAGAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509  
Db 421 ACATGGACAGAGGTGTCTCAAAACGGAAGAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 480  
QY 510 AGTTTCTTTAGCGGACTGGAATGGCTAAACAAATCTGGAACCTTACCCCATATGAT 569  
Db 481 AGTTTCTTTAGCGGACTGGAATGGCTAAACAAATCTGGAACCTTACCCCATATGAT 540  
QY 570 GTGACAAATGCCTAAACAAATTTTCGACAACTATACATCTGGGGGATTCATCACCCG 629  
Db 541 GTGACAAATGCCTAAACAAATTTTCGACAACTATACATCTGGGGGATTCATCACCCG 600  
QY 630 AGCTCAAAACAAACAGCAGACAGAAATTTGATCATCCAGAAATCAGGACAGTAAACAGTCTCA 689

Db 601 AGCTCAAAACAAAGAGCAGACAAAATTTGTATCTCCAAGAAATCAGGACGAGTAACAGTCTCA 660  
QY 690 ACAAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGTTAGGGGT 749  
Db 661 ACAAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGTTAGGGGT 720  
QY 750 CAATCAGGCAGGATAAGCATATATCTGGACCAATTTGTAACACCTGGAGATATCTTAATGATA 809  
Db 721 CAATCAGGCAGGATAAGCATATATCTGGACCAATTTGTAACACCTGGAGATATCTTAACGATA 780  
QY 810 AACAGTAATGCAACTTAGTTGACCCGCGGGATATTTTAAATTTGAAAACAGGGAAGC 869  
Db 781 AACAGTAATGCAACTTAGTTGACCCGCGGGATATTTTAAATTTGAAAACAGGGAAGC 840  
QY 870 TCTGTAATGAGATCAGATGACCCATAGACATTTTGTGTGCTGTAATGTATTACACCAAT 929  
Db 841 TCTGTAATGAGATCAGATGACCCATAGACATTTTGTGTGCTGTAATGTATTACACCAAT 900  
QY 930 GGAAGCATCCCAACGACAAAACCAATTTCAAATGTGAAACAAAGTTTACATATGGAATAATGC 989  
Db 901 GGAAGCATCCCAACGACAAAACCAATTTCAAATGTGAAACAAAGTTTACATATGGAATAATGC 960  
QY 990 CCCAAGTATATCAGGCAAAACACACTTTAAAGCTGGCCACTGGGATCAGGAATATACAGAA 1049  
Db 961 CCCAAGTATATCAGGCAAAACACACTTTAAAGCTGGCCACTGGGATCAGGAATATACAGAA 1020  
QY 1050 AAGCAAAATCAGA 1061  
Db 1021 AAGCAAAATCAGA 1032

Search completed: March 1, 2005, 06:18:12  
Job time : 223 secs

Db 361 GCATCGCTCCGGTCCATTGTAGCATCTCAGGAACATTGGAATTCACACGAGGGGATTC 420  
QY 450 ACATGACAGGTGTCTACTCAAAACGGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509  
Db 421 ACATGACAGGTGTCTACTCAAAACGGAAGTGGATCCTGCAAAAGGGGATCAGCCGAT 480  
QY 510 AGTTTCCTTTAGCCGCTGGAATTTGGCTAACCAAAATCTGGAACCTTTTACCCCAATTTGAAT 569  
Db 481 AGTTTCCTTTAGCCGCTGGAATTTGGCTAACCAAAATCTGGAACCTTTTACCCCAATTTGAAT 540  
QY 570 GTGACAATGCTTAACCAATTAATAATTTTCGCAAACTATACATCTGCGGGGATTCATCACCCG 629  
Db 541 GTGACAATGCTTAACCAATTAATAATTTTCGCAAACTATACATCTGCGGGGATTCATCACCCG 600  
QY 630 AGCTCAAAACACAGCAGACAGAAATTTGTACATCTCAAGAAATCAGGACGAGTAACAGTCTCA 689  
Db 601 AGCTCAAAACACAGCAGACAGAAATTTGTACATCTCAAGAAATCAGGACGAGTAACAGTCTCA 660  
QY 690 ACAAAGAAAGTCAACAAACGATAGTCCCTTAATATCGGATCTAGACCGTGGGTAGGGGT 749  
Db 661 ACAAAGAAAGTCAACAAACATTAATCCCTTAATATCGGATCTAGACCGTGGGTAGGGGT 720  
QY 750 CAAATGAGGAGGATAAGCATATCTGACCAATTTGTAATAACCTGGAGATATCCTTAATGATA 809  
Db 721 CAAATGAGGAGGATAAGCATATCTGACCAATTTGTAATAACCTGGAGATATCCTTAACGATA 780  
QY 810 AACAGTAATGGCACTTAGTTCACCGCGGGGATTTTAAATTTGAAACAGGGAAGC 869  
Db 781 AACAGTAATGGCACTTAGTTCACCGCGGGGATTTTAAATTTGAAACAGGGAAGC 840  
QY 870 TCTGTAATGAGTACAGATGACATGACCCATGATGTTGTCTGATGATGATGATGATGATGATGAT 929  
Db 841 TCTGTAATGAGTACAGATGACATGACCCATGATGATGATGATGATGATGATGATGATGATGAT 900  
QY 930 GGAAGCATCCCCAACGACAAACCAATTTCAAAATGTGAACAAAGTTTACATATGGAATAATGC 989  
Db 901 GGAAGCATCCCCAACGACAAACCAATTTCAAAATGTGAACAAAGTTTACATATGGAATAATGC 960  
QY 990 CCCAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1049  
Db 961 CCCAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1020  
QY 1050 AAGCAATCAGA 1061  
Db 1021 AAGCAATCAGA 1032

RESULT 14  
US-09-762-861B-12  
; Sequence 12, Application US/09762861B  
; Patent No. 6579528  
; GENERAL INFORMATION:  
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher  
; APPLICANT: Education  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-CI-FUS (formerly HKZ-033CFUS)  
; CURRENT APPLICATION NUMBER: US/09/762,861B  
; PRIOR FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 1695  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
US-09-762-861B-12

Query Match 94.7%; Score 1004.8; DB 4; Length 1695;  
Best Local Similarity 98.4%; Pred. No. 2.2e-294;  
Matches 1015; Conservative 0; Mismatches 17; Indels 0; Gaps 0;  
QY 30 ATGAGAGCAACCATTTATTTTGTATCTACTGACCCATTTGGTCTTACAGTCAAAACCCCAACC 89  
Db 1 ATGAGAGCAACCATTTATTTTGTATCTACTGACCCATTTGGTCTTACAGTCAAAACCCCAACC 60  
QY 90 AGTGGAAACACACAGCAGCATTTATGTCTGGGACACCATGACAGTAGCAAAATGGAACATTTG 149  
Db 61 AGTGGCAACACACAGCAGCATTTATGTCTGGGACACCATGACAGTAGCAAAATGGAACATTTG 120  
QY 150 GTAAAAACAATACTGATGACCAAAATTTGAGGTGACAAAATGCTACTCAAAATTTAGTTTCAGAGC 209  
Db 121 GTAAAAACAATACTGATGACCAAAATTTGAGGTGACAAAATGCTACTCAAAATTTAGTTTCAGAGC 180  
QY 210 ATTTCAATAGGGAATAATATGCAACAACTCATATAAAGTTCTTAGATGGAAGAAATTTGCACA 269  
Db 181 ATTTCAATAGGGAATAATATGCAACAACTCATATAAAGTTCTTAGATGGAAGAAATTTGCACA 240  
QY 270 TTAATAGATGCAATCTAGGAGACCCCACTCTGTGATGCTTCCAGTATGAGAAATTTGGGAC 329  
Db 241 TTAATAGATGCAATCTAGGAGACCCCACTCTGTGATGCTTCCAGTATGAGAAATTTGGGAC 300  
QY 330 CTCTTTCATAGAAAGACGAGCGCTTTTTCAGCAATTTCTACCCATATGACATCCCTGACTAT 389  
Db 301 CTCTTTCATAGAAAGACGAGCGCTTTTTCAGCAATTTCTACCCATATGACATCCCTGACTAT 360  
QY 390 GCATCGCTCCGGTCCATTGTAGCATCTCAGGAACATTTAGAAATTTTACAGCAGAGGGATTC 449  
Db 361 GCATCGCTCCGGTCCATTGTAGCATCTCAGGAACATTTAGAAATTTTACAGCAGAGGGATTC 420  
QY 450 ACATGACAGAGTGTCTCACTCAAAACGGAAGTGGAGCCTGCAAAAGGGGATTCAGCCGAT 509  
Db 421 ACATGACAGAGTGTCTCACTCAAAACGGAAGTGGATCTCTGCAAAAGGGAATTCAGCCGAT 480  
QY 510 AGTTTCCTTTAGCCGCTGATTTGGCTTAAACAAATCTGGAACCTTTTACCCCAATTTGAAT 569  
Db 481 AGTTTCCTTTAGCCGCTGATTTGGCTTAAACAAATCTGGAACCTTTTACCCCAATTTGAAT 540  
QY 570 GTGACAATGCTTAACCAATTAATAATTTTGAACAACTATACATCTGGGGGATTCATCACCCG 629  
Db 541 GTGACAATGCTTAACCAATTAATAATTTTGAACAACTATACATCTGGGGGATTCATCACCCG 600  
QY 630 AGCTCAAAACACAGCAGACAGAAATTTGTACATCTCAAGAAATCAGGACGAGTAACAGTCTCA 689  
Db 601 AGCTCAAAACACAGCAGACAGAAATTTGTACATCTCAAGAAATCAGGACGAGTAACAGTCTCA 660  
QY 690 ACAAAGAAAGTCAACAAACGATAGTCCCTTAATATCGGATCTAGACCGTGGGTAGGGGT 749  
Db 661 ACAAAGAAAGTCAACAAACATTAATCCCTTAACATCGGATCTAGACCGTGGGTAGGGGT 720  
QY 750 CAAATGAGGAGGATAAGCATATCTGACCAATTTGTAATAACCTGGAGATATCCTTAATGATA 809  
Db 721 CAAATGAGGAGGATAAGCATATCTGACCAATTTGTAATAACCTGGAGATATCCTTAACGATA 780  
QY 810 AACAGTAATGGCACTTAGTTCACCGCGGGGATTTTAAATTTGAAACAGGGAAGC 869  
Db 781 AACAGTAATGGCACTTAGTTCACCGCGGGGATTTTAAATTTGAAACAGGGAAGC 840  
QY 870 TCTGTAATGAGTACAGATGACATGACCCATGATGTTGTCTGATGATGATGATGATGATGATGAT 929  
Db 841 TCTGTAATGAGTACAGATGACATGACCCATGATGATGATGATGATGATGATGATGATGATGAT 900  
QY 930 GGAAGCATCCCCAACGACAAACCAATTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 989  
Db 901 GGAAGCATCCCCAACGACAAACCAATTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 960  
QY 990 CCCAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1049  
Db 961 CCCAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1020  
QY 1050 AAGCAATCAGA 1061

```
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2740
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 300:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1762 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-458-101-300

Query Match 96.0%; Score 1018.4; DB 1; Length 1762;
Best Local Similarity 97.5%; Pred. No. 1.7e-298;
Matches 1034; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1 AGCAAAAGCAGGGGATTTCTGTCAATCATCAAGACCAACCATTTTGTACTACTGA 60
DB 1 AGCAAAAGCAGGGGATTTCTGTCAATCATCAAGACCAACCATTTTGTACTACTGA 60
QY 61 CCCATTGGGTCTACAGTCAAAACCCCAACAGTGGAAACAAACAGCCACATTATCTGG 120
DB 61 CCCATTGGGTCTACAGTCAAAACCCCAACAGTGGAAACAAACAGCCACATTATCTGG 120
QY 121 GACACATGCTAGCAATGAACATTTGGTAAAAACAATACTGATGACCAATTTGAGG 180
DB 121 GACACATGCTAGCAATGAACATTTGGTAAAAACAATACTGATGACCAATTTGAGG 180
QY 181 TCACAAATGCTAGTAAATTTAGTTCAGAGCATTTCAATGGGAAATATGCAACATCAT 240
DB 181 TCACAAATGCTAGTAAATTTAGTTCAGAGCATTTCAATGGGAAATATGCAACATCAT 240
QY 241 ATAAAGTCTTAGATGAAAGAAATTTGCAATTAATAGATCAATGCTAGGAGACCCCACT 300
DB 241 ATAGGTTCTAGATGAAAGAAATTTGCAATTAATAGATCAATGCTAGGAGACCCCACT 300
QY 301 GTGATGCTTCAGTATGAAATTTGGGACCTCTTCATGAAAGAGCAGCGCTTTCAGCA 360
DB 301 GTGATGCTTCAGTATGAAATTTGGGACCTCTTCATGAAAGAGCAGCGCTTTCAGCA 360
QY 361 ATTGCTACCCATATGACATCCCTGACTATGATCGCTCCGCTCCATTTGAGCATCCTCAG 420
DB 361 ATTGCTACCCATATGACATCCCTGACTATGATCGCTCCGCTCCATTTGAGCATCCTCAG 420
QY 421 GAACATTTAGAAATTCACAGCAGAGGGATTCAATGAGCAGGTGTCACTCAAAACGGAGAA 480
DB 421 GAACATTTAGAAATTCACAGCAGAGGGATTCAATGAGCAGGTGTCACTCAAAACGGAGAA 480
QY 481 GTGGAGCTTGCAAAAGGGGATCAGCGGATAGTTTCTTTAGCGGACTGAATTTGGCTAAACA 540
DB 481 GTGGAGCTTGCAAAAGGGGATCAGCGGATAGTTTCTTTAGCGGACTGAATTTGGCTAAACA 540
QY 541 AATCTGGAATCTTTACCCCAATTTGAATGTGCAATGCTCAACATTAATAAATTTTCGACA 600
DB 541 AATCTGGAATCTTTACCCCAATTTGAATGTGCAATGCTCAACATTAATAAATTTTCGACA 600
QY 601 AACTATACATCTGGGGATTTCACTACCCGAGTCAAAACCAACAGCAGACAGAAATTTGTACA 660
DB 601 AACTATACATCTGGGGATTTCACTACCCGAGTCAAAACCAACAGCAGACAGAAATTTGTATA 660
QY 661 TCAAGAATTCAGGACAGGTAACAGTCTCAAAAAAGAAAGTCAACAGATAGTCCCTTA 720
DB 661 TCAAGAATTCAGGACAGGTAACAGTCTCAACAGAAAGAAAGTCAACAGATAGTCCCTTA 720
QY 721 ATATCGGATCTAGCCGCTGGGTAGGGTCAATCAGGAGGATAGCATATATCTGACCA 780
DB 721 ATATCGGATCTAGCCGCTGGGTAGGGTCAATCAGGAGGATAGCATATATCTGACCA 780
QY 781 TTGTAAACCTTGAGATATCTTAATGATAAAGTAAATGGCAACTTTAGTTGACCGCGGG 840
```

```
DB 781 TTGTAAACCTTGAGATATCTTAACGATAAAACAGTAATGGCACTTAGTTGCACCGCGG 840
QY 841 GATATTTTAAATTTGAACACAGGAAAGCTCTGTAATGAGATCAGATGACCCATAGACA 900
DB 841 GATATTTTAAATTTGAACACAGGAAAGCTCTGTAATGAGATCAGATGACCCATAGACA 900
QY 901 TTGTGTCTCTGAATGTATTACACAAATGGAAGCATCCCAACGACAAACCATTTTCAA 960
DB 901 CTGTGTCTCTGAATGTATTACACAAATGGAAGCATCCCAACGACAAACCATTTTCAA 960
QY 961 ATGTGAACAAAGTTACATATGGAATAATCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
DB 961 ATGTGAACAAAGTTACATATGGAATAATCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
QY 1021 TGGCCACTGGGATGAGGATATACCAAAAGCAATCAGA 1061
DB 1021 TGGCCACTGGGATGAGGATATACCAAAAGCAATCAGA 1061

RESULT 13
US-09-506-286B-12
; Sequence 12, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 12
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-12

Query Match 94.7%; Score 1004.8; DB 4; Length 1695;
Best Local Similarity 98.4%; Pred. No. 2.2e-294;
Matches 1015; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 30 ATGAAGACAACCATTTATTTGTACTACTGACCCCAATTTGGGTCTACAGTCAAAACCAACC 89
DB 1 ATGAAGACAACCATTTATTTGTACTACTGACCCCAATTTGGGTCTACAGTCAAAACCAACC 60
QY 90 AGTGAACAAACACAGCCACATTTATGTTCTGGGACCAATGCGAGTAGCAAAATGGAACTTG 149
DB 61 AGTGAACAAACACAGCCACATTTATGTTCTGGGACCAATGCGAGTAGCAAAATGGAACTTG 120
QY 150 GTAAAAACAATAACTGTAGTACCAATTCAGGTGACAAATGCTACTGAAATAGTTTCAGAGC 209
DB 121 GTAAAAACAATAACTGTAGTACCAATTCAGGTGACAAATGCTACTGAAATAGTTTCAGAGC 180
QY 210 ATTTCAATAGGGAATAATATGCAACATTCATATAAGTTCTAGATGGAGAAATTCGACA 269
DB 181 ATTTCAATAGGGAATAATATGCAACATTCATATAAGTTCTAGATGGAGAAATTCGACA 240
QY 270 TTAATAGATGCAATGCTAGGAGACCCCACTGTGTGATGTTCTCCAGTATGAGAAATTTGGAC 329
DB 241 TTAATAGATGCAATGCTAGGAGACCCCACTGTGTGATGTTCTCCAGTATGAGAAATTTGGAC 300
QY 330 CTCCTTCATAGAAAGAGCAGCGCTTTTCAGCAATTCCTACCCATATGACATCCCTGACTAT 389
DB 301 CTCCTTCATAGAAAGAGCAGCGCTTTTCAGCAATTCCTACCCATATGACATCCCTGACTAT 360
QY 390 GCATCGCTCCGCTCCATTTGTAGCATCTTCAGGAAATTAAGAAATTCACAGCAGAGGATTC 449
```

STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/709,209  
FILING DATE: 21-AUG-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/105,483  
FILING DATE: 12-AUG-1993  
APPLICATION NUMBER: US 07/847,951  
FILING DATE: 06-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer, William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 300:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1762 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-709-209-3d0

Query Match 96.0%; Score 1018.4; DB 1; Length 1762;  
Best Local Similarity 97.5%; Pred. No. 1.7e-298;  
Matches 1034; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1 AGCAAAAGCAGGGGATATTTCTCAATCATGAAGACAACCACTATTATTTGATCTACTGA 60  
DB 1 AGCAAAAGCAGGGGATATTTCTCAATCATGAAGACAACCACTATTATTTGATCTACTGA 60  
QY 61 CGCATTTGGGTCTACAGTCAAAACCCCAACCAAGTGGAAACCAACAGCAGCAATTATGCTGG 120  
DB 61 CCCATTGGGTCTACAGTCAAAACCCCAACCAAGTGGCAACCAACAGCAGCAATTATGCTGG 120  
QY 121 GACACCATCAGTAGCAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 180  
DB 121 GACACCATCAGTAGCAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 180  
QY 181 TGACAAATGCTACTGATTAATGATTTGAGAGCAATTTCAATAGGGAATATGCAACCACTCAT 240  
DB 181 TGACAAATGCTACTGATTAATGATTTGAGAGCAATTTCAATAGGGAATATGCAACCACTCAT 240  
QY 241 ATAAAGTTCTAGATGAAGAAATTTGACATTAATAGATGAATGCTAGAGAGACCCCACT 300  
DB 241 ATAGGGTTCTAGATGAAGAAATTTGACATTAATAGATGAATGCTAGAGAGACCCCACT 300  
QY 301 GTGATCTCTCCAGTATGGAATTTGGAGCTCTTTCATAGAAAGCAGCGCTTTTCAGCA 360  
DB 301 GTGATCTCTCCAGTATGGAATTTGGAGCTCTTTCATAGAAAGCAGCGCTTTTCAGCA 360  
QY 361 ATTGCTACCAATATGATCACTCCCTGACTATGATCGCTCCGGTCCATTTGATGATCTCTCAG 420  
DB 361 ATTGCTACCAATATGATCACTCCCTGACTATGATCGCTCCGGTCCATTTGATGATCTCTCAG 420  
QY 421 GAACATTAGAAATTCACAGCAGAGGGATTCACATGGAAGAGTGTCTCAAAACCGGAAGAA 480  
DB 421 GAACATTAGAAATTCACAGCAGAGGGATTCACATGGAAGAGTGTCTCAAAACCGGAAGAA 480  
QY 481 GTGAGCCTGCAAAAGGGATCAGCCGATGTTCTTTAGCCGACCTGAATTTGCTTAACAA 540  
DB 481 GTGAGCCTGCAAAAGGGATCAGCCGATGTTCTTTAGCCGACCTGAATTTGCTTAACAA 540  
QY 541 AATCTGGAAACTCTTACCCTCCACATTTGAATGTGCAATGCTCAATAAAAAATTTTCGACA 600

DB 541 AATCTGGAAATCTTTACCCCATATTGAATGTGCAATGCTCAATAAAAAATTTTCGATA 600  
QY 601 AACTATACATCTGGGGATTTCTACCCGAGTCTCAAAACCAAGCAGCAGAGATTTGTACA 660  
DB 601 AACTATACATCTGGGGATTTCTACCCGAGTCTCAAAACCAAGCAGCAGAGATTTGTATA 660  
QY 661 TCCAGAATCAGAGCAGGTAACAGTCTCAAAAGAAAGAGTCAACAAACAGTAAATCCCTA 720  
DB 661 TCCAGAATCAGAGCAGGTAACAGTCTCAAAAGAAAGAGTCAACAAACAGTAAATCCCTA 720  
QY 721 ATATCGGATCTAGACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 780  
DB 721 ACATCGGATCTAGACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 780  
QY 781 TTGTAAACCTGGAGATATCTTAATGATTAACAGTAAATGCGCACTTTAGTTGACCGCGGG 840  
DB 781 TTGTAAACCTGGAGATATCTTAACAGTAAATGCGCACTTTAGTTGACCGCGGG 840  
QY 841 GATATTTAAATTTGAAACAGGGAAGAGCTCTGTAATGAGATCAGATGCAACCATAGACA 900  
DB 841 GATATTTAAATTTGAAACAGGGAAGAGCTCTGTAATGAGATCAGATGCAACCATAGACA 900  
QY 901 TTTGTGTCTGATGATTTATTAACCAAAATGGAAGCATCCCAACGACAAACCACTTTCAA 960  
DB 901 CTTGTGTCTGATGATTTATTAACCAAAATGGAAGCATCCCAACGACAAACCACTTTCAA 960  
QY 961 ATGTGAACAAAGTTACATATGGAATGCGCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020  
DB 961 ATGTGAACAAAGTTACATATGGAATGCGCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020  
QY 1021 TGGCCACTGGGATGAGGATATATACCAAGAAACCAATCAGA 1061  
DB 1021 TGGCCACTGGGATGAGGATATATACCAAGAAACCAATCAGA 1061

RESULT 12  
US-08-458-101-300  
Sequence 300, Application US/08458101  
Patent No. 5765599  
GENERAL INFORMATION:  
APPLICANT: Paolletti, Enzo  
APPLICANT: Perkus, Marion E.  
APPLICANT: Taylor, Jill  
APPLICANT: Tartaglia, James  
APPLICANT: No. 5765599ton, Elizabeth K.  
APPLICANT: Riviere, Michel  
APPLICANT: de Taisne, Charles  
APPLICANT: Limbach, Keith J.  
APPLICANT: Johnson, Gerard P.  
APPLICANT: Pincus, Steven E.  
APPLICANT: Cox, William I.  
APPLICANT: Audonnet, Jean-Christophe Francis  
APPLICANT: Gattig, Russell Robert  
ADDRESSEE: c/o William S. Frommer  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,101  
FILING DATE: 01-JUN-1995

Db 901 GGAAGCATCCCAAGCAGCAAAACCAATTTCAAAATGTGAACAAAGTTACATATGGAATAATGC 960  
Qy 990 CCCAAGTATATCAGCAGCAAAACCACTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1049  
Db 961 CCCAAGTATATCAGCAGCAAAACCACTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1020  
Qy 1050 AAGCAAAATCAGA 1061  
Db 1021 AAGCAAAATCAGA 1032

## RESULT 10

US-08-105-483-300  
; Sequence 300, Application US/08105483  
; Patent No. 5494807  
; GENERAL INFORMATION:  
; APPLICANT: Paolletti, Enzo  
; TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE  
; TITLE OF INVENTION: STRAIN  
; NUMBER OF SEQUENCES: 462  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Curtis, Morris & Safford  
; ADDRESSEE: c/o William S. Frommer  
; STREET: 530 Fifth Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/105,483  
; FILING DATE: 12-AUG-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/847,951  
; FILING DATE: 06-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Frommer, William S.  
; REGISTRATION NUMBER: 25,506  
; REFERENCE/DOCKET NUMBER: 454310-2400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 840-3333  
; TELEFAX: (212) 840-0712  
; INFORMATION FOR SEQ ID NO: 300:  
; SEQUENCE CHARACTERISTICS:  
; TYPE: nucleic acid  
; LENGTH: 1762 base pairs  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-105-483-300

Query Match 96.0%; Score 1018.4; DB 1; Length 1762;

Best Local Similarity 97.5%; Pred. No. 1.7e-298;

Matches 1034; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 1 AGCAAAAGCAGGGGATATTTCTGTCATCATGAGCAACCAATTTATTTGATACACTGA 60  
Db 1 AGCAAAAGCAGGGGATATTTCTGTCATCATGAGCAACCAATTTATTTGATACACTGA 60  
Qy 61 CCCATTGGTCTACAGTCAAAACCCCAACCAAGTGGGAACCAACGCCACATTTGCTGG 120  
Db 61 CCCATTGGTCTACAGTCAAAACCCCAACCAAGTGGGAACCAACGCCACATTTGCTGG 120  
Qy 121 GACACCATGAGTAGCAAAATGGAACATTTGGTAAAAACAATACTGATGACCAAAATTTGAGG 180  
Db 121 GACACCATGAGTAGCAAAATGGAACATTTGGTAAAAACAATACTGATGACCAAAATTTGAGG 180  
Qy 181 TGCAAAATCCTACTGATTAATTTAGTTCAGAGCAATTTCAATAGGGAAATATGCAACAATCAT 240

Db 181 TGCAAAATCCTACTGATTAATTTAGTTCAGAGCAATTTCAATAGGGAAATATGCAACAATCAT 240  
Qy 241 ATAAAGTTCTAGATGGAAGAAATTTGCACATTAATAGATGCAATGCTAGGAGACCCCTACT 300  
Db 241 ATAGGGTTCTAGATGGAAGAAATTTGCACATTAATAGATGCAATGCTAGGAGACCCCTACT 300  
Qy 301 GTGATGCTCTCCAGTATGAGAAATTTGGGACCTCTTTTCATAGAAAGAGCAGCGCTTTTCAGA 360  
Db 301 GTGATGCTCTCCAGTATGAGAAATTTGGGACCTCTTTTCATAGAAAGAGCAGCGCTTTTCAGA 360  
Qy 361 ATTGCTACCATATGACATCCCTGACTATGATGCTCCGGTCCATTTGTAGCATCTCTCAG 420  
Db 361 ATTGCTACCATATGACATCCCTGACTATGATGCTCCGGTCCATTTGTAGCATCTCTCAG 420  
Qy 421 GAACATTAGAATTTACAGCAGAGGATTTACATGAGCAGAGGTGTCTACTCAAAACGGAAGAA 480  
Db 421 GAACATTAGAATTTACAGCAGAGGATTTACATGAGCAGAGGTGTCTACTCAAAACGGAAGAA 480  
Qy 481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTTAGCCGACTGAATTTGGCTAAACA 540  
Db 481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTTAGCCGACTGAATTTGGCTAAACA 540  
Qy 541 AATCTGGAATCTTTACCCCATATTTGAATGTGACATGCTTAACATTAATAAATTTTCGATA 600  
Db 541 AATCTGGAATCTTTACCCCATATTTGAATGTGACATGCTTAACATTAATAAATTTTCGATA 600  
Qy 601 AACTATACATCTGGGGGATTCATCACCAGCTCAAAACCAACAGCAGACAGAAATTTGTACA 660  
Db 601 AACTATACATCTGGGGGATTCATCACCAGCTCAAAACCAACAGCAGACAGAAATTTGTATA 660  
Qy 661 TCCAAGATCAGGACGAGTAACAGTCTCAACAAAGAAAGTCAACAAACAGTAAATCCCTTA 720  
Db 661 TCCAAGATCAGGACGAGTAACAGTCTCAACAAAGAAAGTCAACAAACAGTAAATCCCTTA 720  
Qy 721 ATATCGGATCTAGACCGTGGGTGAGGTGCTCAATCAGGAGGATAGCATATCTAGTGACA 780  
Db 721 ACATCGGATCTAGACCGTGGGTGAGGTGCTCAATCAGGAGGATAGCATATCTAGTGACA 780  
Qy 781 TTGTAAAACCTGGAGATATCTCAATGATAAAACAGTAATGGCAACTTAGTTGACCCGCGG 840  
Db 781 TTGTAAAACCTGGAGATATCTCAACGATTAACAGTAAACAGTAAATGGCAACTTAGTTGACCCGCGG 840  
Qy 841 GATATTTTAAATGAAAAACAGGAAAGCTCTGTAATGAGATCAGATGCAACCCATAGACA 900  
Db 841 GATATTTTAAATGAGAAACAGGAAAGCTCTGTAATGAGATCAGATGCAACCCATAGACA 900  
Qy 901 TTTGTGCTCTGAATGATTTACACCAATGGAAGCATCCCAACAGCAAAACCATTTTCAA 960  
Db 901 CTTGTGCTCTGAATGATTTACACCAATGGAAGCATCCCAACAGCAAAACCATTTTCAA 960  
Qy 961 ATGTGAACAAAGTTTACATATGGAATAATGCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020  
Db 961 ATGTGAACAAAGTTTACATATGGAATAATGCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020  
Qy 1021 TGGCCACTGGGATGAGGAATATACAGAAAAAGCAAAATCAGA 1061  
Db 1021 TGGCCACTGGGATGAGGAATATACAGAAAAAGCAAAATCAGA 1061

## RESULT 11

US-08-709-209-300  
; Sequence 300, Application US/08709209  
; Patent No. 5762938  
; GENERAL INFORMATION:  
; APPLICANT: Paolletti, Enzo  
; TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE  
; TITLE OF INVENTION: STRAIN  
; NUMBER OF SEQUENCES: 462  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Curtis, Morris & Safford  
; ADDRESSEE: c/o William S. Frommer  
; STREET: 530 Fifth Avenue  
; CITY: New York

```
181 TGACAAATGCTACTGAATAGTTTACAGCATTTTCAATAGGAAATATCAACAATCAT 240
241 ATAAAGTTCTAGATGGAAGAAATGACATTAATAGATGCAATGCTAGGAGACCCCACT 300
241 ATAGAGTTCTAGATGGAAGAAATGACATTAATAGATGCAATGCTAGGAGACCCCACT 300
301 GTGATGCTTCCAGTATGAGAAATGGAAGCTTCTCATAGAAAGAGACGCGTTTCAGCA 360
301 GTGATGCTTCCAGTATGAGAAATGGAAGCTTCTCATAGAAAGAGACGCGTTTCAGCA 360
361 ATTGCTTACCATATGATACCTCGCTGCTATGCTATGCTATGCTATGCTATGCTATGCT 420
361 GTTGTCTACCATATGATACCTCGCTGCTATGCTATGCTATGCTATGCTATGCTATGCT 420
421 GAACATTAGAAATTCACAGAGAGGGAATTCACATGAGACAGGTGTCTCAAAAGGAGAA 480
421 GAACATTAGAAATTCACAGAGAGGGAATTCACATGAGACAGGTGTCTCAAAAGGAGAA 480
481 GTGGAGCTGCAAAAGGGGATCAGCGATAGTTTCTTTAGCCGACTGAATTCGCTAACAA 540
481 GTGGAGCTGCAAAAGGGGATCAGCGATAGTTTCTTTAGCCGACTGAATTCGCTAACAA 540
541 AATCTGGAATCTTACCCCACTTGAATGTGCAATGCTTAACTAATAAAATTTTCGACA 600
541 AATCTGGAATCTTACCCCACTTGAATGTGCAATGCTTAACTAATAAAATTTTCGACA 600
601 AATCTGGAATCTTACCCCACTTGAATGTGCAATGCTTAACTAATAAAATTTTCGACA 660
601 AATCTGGAATCTTACCCCACTTGAATGTGCAATGCTTAACTAATAAAATTTTCGACA 660
661 TCCAGAAATCAGACAGGATGAGTCTCAACAAAGAGAGTCAACAAAGAGATAGTCCCTA 720
661 TCCAGAAATCAGACAGGATGAGTCTCAACAAAGAGAGTCAACAAAGAGATAGTCCCTA 720
721 ATATCGGATCTAGACCGTGGGTAGGGGTCAATCAGCGAGGATAGCATATATCTGACCA 780
721 ATATCGGATCTAGACCGTGGGTAGGGGTCAATCAGCGAGGATAGCATATATCTGACCA 780
781 TTGTAAATCTGAGATATCTTAATGATAACAGTATGCTATGCTATGCTATGCTATGCT 840
781 TTGTAAATCTGAGATATCTTAATGATAACAGTATGCTATGCTATGCTATGCTATGCT 840
841 GATATTTAAATTTGAAAACAGGGAAGGCTCTGTATGATGATGATGATGATGATGATG 900
841 GATATTTAAATTTGAAAACAGGGAAGGCTCTGTATGATGATGATGATGATGATGATG 900
901 TTGTGTGTCTGAATGATTTACACCAATGGAAGCATCCCAACGACAAACCAATTTCAA 960
901 TTGTGTGTCTGAATGATTTACACCAATGGAAGCATCCCAACGACAAACCAATTTCAA 960
961 ATGTGAACAAAGTATCATATGGAATGCCCCAAGTATATCAGGCAAAACATTTAAAGC 1020
961 ATGTGAACAAAGTATCATATGGAATGCCCCAAGTATATCAGGCAAAACATTTAAAGC 1020
1021 TGCCCACTGGATGAGAAATATACCAAGAAAGCAAAATCAGA 1061
1021 TGCCCACTGGATGAGAAATATACCAAGAAAGCAAAATCAGA 1061
```

## RESULT 9

```
US-09-622-951-1
; Sequence 1, Application US/09622951
; Patent No. 6713068
; GENERAL INFORMATION:
; APPLICANT: JEAN CHRISTOPHE AUDONNET ET AL.
; TITLE OF INVENTION: LIVE RECOMBINED VACCINES INJECTED WITH ADJUVANT
; FILE REFERENCE: 454313-3159
; CURRENT APPLICATION NUMBER: US/09/622,951
; CURRENT FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: PCT/FR99/00453
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 31
```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1698
; TYPE: DNA
; ORGANISM: Equine Influenza Virus, Newmarket 2/93 Strain
US-09-622-951-1
```

```
Query Match 96.1%; Score 1019.2; DB 4; Length 1698;
Best Local Similarity 99.2%; Pred. No. 9.5e-299;
Matches 1024; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 30 ATGAAGACAACCATTTATTTGATCTACTACCCATTTGGGTCTACAGTCAAAACCCAAACC 89
DB 1 ATGAAGACAACCATTTATTTGATCTACTACCCATTTGGGTCTACAGTCAAAACCCAAACC 60
QY 90 AGTGAACAACAACAGCCACATTTATGCTGGGACCACTGAGTACAGTACAGTACAGTACAGT 149
DB 61 AGTGAACAACAACAGCCACATTTATGCTGGGACCACTGAGTACAGTACAGTACAGTACAGT 120
QY 150 GTAAAAACAATACTGATGACCAAAATTCAGGTGACAAATGCTTACTGAAATTTAGTTCAGAGC 209
DB 121 GTAAAAACAATACTGATGACCAAAATTCAGGTGACAAATGCTTACTGAAATTTAGTTCAGAGC 180
QY 210 ATTTCAATAGGGAATAATGCAACAATCTCATATAAAGTTCTAGATGGAAGAAATTCGACA 269
DB 181 ATTTCAATAGGGAATAATGCAACAATCTCATATAAAGTTCTAGATGGAAGAAATTCGACA 240
QY 270 TTAATAGATGCAATGCTAGGAGACCCCACTGCTGATGCTTCCAGTATGAGAAATTTGGGAC 329
DB 241 TTAATAGATGCAATGCTAGGAGACCCCACTGCTGATGCTTCCAGTATGAGAAATTTGGGAC 300
QY 330 CTCCTTCATAGAAAGAGCAGCGCTTTTCAGCAATTCCTACCCATATGACATCCCTGACTAT 389
DB 301 CTCCTTCATAGAAAGAGCAGCGCTTTTCAGCAATTCCTACCCATATGACATCCCTGACTAT 360
QY 390 GCATCGCTCCGGTCCATTGTAGTACCTCAGGAAATTCAGGAAATTCAGGAGAGGGAATTC 449
DB 361 GCATCGCTCCGGTCCATTGTAGTACCTCAGGAAATTCAGGAAATTCAGGAGAGGGAATTC 420
QY 450 ACATCGACAGGTGTCTCACTCAAAACGGAAGAGTGGAGCTGCAAAAGGGGATTCAGCCGAT 509
DB 421 ACATCGACAGGTGTCTCACTCAAAACGGAAGAGTGGAGCTGCAAAAGGGGATTCAGCCGAT 480
QY 510 AGTTCTTTTAGCCGACTGAATTTGGCTAACAAATCTGGAATCTTACCCCACTTTGAAT 569
DB 481 AGTTCTTTTAGCCGACTGAATTTGGCTAACAAATCTGGAATCTTACCCCACTTTGAAT 540
QY 570 GTGCAATGCTTAAACAATAAATTTTGACAAATCTATACATCTGGGGATTCATCCCGG 629
DB 541 GTGCAATGCTTAAACAATAAATTTTGACAAATCTATACATCTGGGGATTCATCCCGG 600
QY 630 AGCTCAAAACCAACAGCAGCAAGATTTGTACATCCCAAGATCAGGACGAGTAAACAGTCTCA 689
DB 601 AGCTCAAAACCAACAGCAGCAAGATTTGTACATCCCAAGATCAGGACGAGTAAACAGTCTCA 660
QY 690 ACAAAGAAAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGGTGGGTAGGGGT 749
DB 661 ACAAAGAAAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGGTGGGTAGGGGT 720
QY 750 CAATCAGGAGGATAGCATATCTGAGCAATTTGTAACCTGGAGATATCTCTAATGATA 809
DB 721 CAATCAGGAGGATAGCATATCTGAGCAATTTGTAACCTGGAGATATCTCTAATGATA 780
QY 810 AACAGTATGCAACTTAGTTGACCGGGGATATTTTAAATTTGAAAACAGGGAAGC 869
DB 781 AACAGTATGCAACTTAGTTGACCGGGGATATTTTAAATTTGAAAACAGGGAAGC 840
QY 870 TCTGTAATGAGATCAGATGACCCATAGACATTTGTGTCTGAAATGTAATACCAAT 929
DB 841 TCTGTAATGAGATCAGATGACCCATAGACATTTGTGTCTGAAATGTAATACCAAT 900
QY 930 GGAAGCATCCCAACGACAAACATTTCAAAATGGAAGTATCATATGGAAGATGC 989
```

GENERAL INFORMATION:  
APPLICANT: Dowling, Patricia W.  
APPLICANT: Youngner, Julius S.  
TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
FILE REFERENCE: EQ-1-C2-1  
CURRENT APPLICATION NUMBER: US/10/065,133A  
CURRENT FILING DATE: 2002-12-10  
PRIOR APPLICATION NUMBER: PCT/US99/18583  
PRIOR FILING DATE: 1999-08-12  
PRIOR APPLICATION NUMBER: 09/133,921  
PRIOR FILING DATE: 1998-08-13  
NUMBER OF SEQ ID NOS: 108  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 7  
LENGTH: 1762  
TYPE: DNA  
ORGANISM: Equine influenza virus H3N8  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (30)..(1724)  
OTHER INFORMATION:  
US-10-065-133A-7

Query Match 97.3%; Score 1032.2; DB 4; Length 1762;

Best Local Similarity 98.3%; Pred. No. 1.1e-302;

Mismatches 0; Conservative 0; Indels 0; Gaps 0;

QY 1 AGCAAAAGCAGGGGATTTCTGTCATCATCAAGACCAACCATTTTGTACTACTGA 60  
DB 1 AGCAAAAGCAGGGGATTTCTGTCATCATCAAGACCAACCATTTTGTACTACTGA 60  
QY 61 CCCATTGGGCTACAGTCAAAACCCCAACCCAGTGGAAACACACAGCCACATTATGCTGG 120  
DB 61 CCCATTGGGCTACAGTCAAAACCCCAACCCAGTGGAAACACACAGCCACATTATGCTGG 120  
QY 121 GACACATGTCAGTACCAATGGAACATTGGTAAACCAATTAATGATGACCAATTTGAGG 180  
DB 121 GACACATGTCAGTACCAATGGAACATTGGTAAACCAATTAATGATGACCAATTTGAGG 180  
QY 181 TGACAAATGCTACTGAATTTAGTTCAGAGCATTTCAATAGGAAATATGCAACACTCAT 240  
DB 181 TGACAAATGCTACTGAATTTAGTTCAGAGCATTTCAATAGGAAATATGCAACACTCAT 240  
QY 241 ATAAAGTCTTAGATGGAAGAAATTTGCAATTAATAGATGCAATGCTAGGAGACCCCACT 300  
DB 241 ATAGAGTCTTAGATGGAAGAAATTTGCAATTAATAGATGCAATGCTAGGAGACCCCACT 300  
QY 301 GTGATGCTTCCAGTATGAGAAATTTGGACCTCTTCATGAAAGAGAGCGGCTTTTCAGCA 360  
DB 301 GTGATGCTTCCAGTATGAGAAATTTGGACCTCTTCATGAAAGAGAGCGGCTTTTCAGCA 360  
QY 361 ATTGCTACCCATATGACATCCCTGACTATGATCGCTCCGTCCTATGTCATCTCTCAG 420  
DB 361 GTTGTACCCATATGACATCCCTGACTATGATCGCTCCGTCCTATGTCATCTCTCAG 420  
QY 421 GAACATTTAGAAATTCACAGCAGAGGGATTCACATGGAAGAGTGTCACTCAAAACGGAAGAA 480  
DB 421 GAACATTTAGAAATTCACAGCAGAGGGATTCACATGGAAGAGTGTCACTCAAAACGGAAGAA 480  
QY 481 GTGGAGCTTGAAAGGGGATGACCGGATAGTTTCTTTAGCGGACTGAATTTGGCTTAACAA 540  
DB 481 GTGGATCTTGCAAAAGGGGATGACCGGATAGTTTCTTTAGCGGACTGAATTTGGCTTAACAG 540  
QY 541 AATCTGAAACTCTTACCCCAATTTGAATGTGCAATGCTTAACTAAATTTTCGACA 600  
DB 541 AATCTGAAACTCTTACCCCAATTTGAATGTGCAATGCTTAACTAAATTTTCGACA 600  
QY 601 AACTATACATCTGGGGATTTATCACCAGGCTCAACCAACAGCAGACAGAAATTTGTACA 660  
DB 601 AACTATACATCTGGGGATTTATCACCAGGCTCAACCAACAGCAGACAGAAATTTGTACA 660  
QY 661 TCAAGAAATCAGACAGGTAAAGTCTCTCAACAAAGAGAGTCAACAAAGATAGTCCCTTA 720  
DB 661 TCAAGAAATCAGACAGGTAAAGTCTCTCAACAAAGAGAGTCAACAAAGATAGTCCCTTA 720

DB 661 TCCAGAAATCGGACGAGTAAACAGTCTCAACAAAGAAAGTCAACAAATAATCCCTTA 720  
QY 721 ATATCGGATCTAGACCGTGGGTAGGGGTCAATCAGGCGAGGATAGCATATATCTGACCA 780  
DB 721 ACATCGGATCTAGACCGGCGGTGAGGGGTCAATCAGGCGAGGATAGCATATATCTGACCA 780  
QY 781 TTGTAAAAACCTGGAGATATCTTAATGATAAACAAGTAAATGGCAACTTACTTGCACCGGG 840  
DB 781 TTGTAAAAACCTGGAGATATCTTAATGATAAACAAGTAAATGGCAACTTACTTGCACCGGG 840  
QY 841 GATATTTTAAATTTGAAAACAGGAAAGCTCTGTAATGAGATCAGATGACCCATAGACA 900  
DB 841 GATATTTTAAATTTGAAAACAGGAAAGCTCTGTAATGAGATCAGATGACCCATAGACA 900  
QY 901 TTTGTGTCTGTAATTTACACCAATGAAGCATCCCAACGACCAAAACCATTTTCAA 960  
DB 901 TTTGTGTCTGTAATTTACACCAATGAAGCATCCCAACGACCAAAACCATTTTCAA 960  
QY 961 ATGTGAACAAAGTTACATATGGAATAATGCCCAAGTATATCAGGCAAAACACTTTTAAAGC 1020  
DB 961 ATGTGAACAAAGTTACATATGGAATAATGCCCAAGTATATCAGGCAAAACACTTTTAAAGC 1020  
QY 1021 TGGCCACTGGATGAGGATATACAGAAAGCAATCAGA 1061  
DB 1021 TGGCCACTGGATGAGGATATACAGAAAGCAATCAGA 1061

## RESULT 8

US-10-434-811A-7

; Sequence 7, Application US/10434811A

; Patent No. 6824784

; GENERAL INFORMATION:

; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher

; APPLICANT: Education

; APPLICANT: Dowling, Patricia W.

; APPLICANT: Youngner, Julius S.

; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES

; FILE REFERENCE: EQ-1-C1-PUS-1

; CURRENT APPLICATION NUMBER: US/10/434,811A

; CURRENT FILING DATE: 2003-05-08

; PRIOR APPLICATION NUMBER: PCT/US99/18583

; PRIOR FILING DATE: 1999-08-12

; PRIOR APPLICATION NUMBER: 09/133,921

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 7

; LENGTH: 1762

; TYPE: DNA

; ORGANISM: Equine influenza virus H3N8

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (30)..(1724)

; OTHER INFORMATION:

US-10-434-811A-7

Query Match

Best Local Similarity 97.3%; Score 1032.2; DB 4; Length 1762;

Mismatches 1043; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 AGCAAAAGCAGGGGATTTCTGTCATCATCAAGACCAACCATTTTGTACTACTGA 60  
DB 1 AGCAAAAGCAGGGGATTTCTGTCATCATCAAGACCAACCATTTTGTACTACTGA 60  
QY 61 CCCATTGGGCTACAGTCAAAACCCCAACCCAGTGGAAACACACAGCCACATTATGCTGG 120  
DB 61 CCCATTGGGCTACAGTCAAAACCCCAACCCAGTGGAAACACACAGCCACATTATGCTGG 120  
QY 121 GACACATGTCAGTACCAATGGAACATTGGTAAACCAATTAATGATGACCAATTTGAGG 180  
DB 121 GACACATGTCAGTACCAATGGAACATTGGTAAACCAATTAATGATGACCAATTTGAGG 180  
QY 181 TGACAAATGCTACTGAATTTAGTTCAGAGCATTTTCAATAGGAAATATGCAACACTCAT 240  
DB 181 TGACAAATGCTACTGAATTTAGTTCAGAGCATTTTCAATAGGAAATATGCAACACTCAT 240

Db 541 AATCTGGAACCTCTTACCCACATGAAATGAGCAATGCTTAACTATAAATTTGAC 600  
QY 601 AACTATACATCTGGGGATTCATCACCAGAGCTCAAAACCAACAGACAGAGAAATGTACA 660  
Db 601 AACTATACATCTGGGGATTCATCACCAGAGCTCAAAACCAACAGACAGAGAAATGTACA 660  
QY 661 TCCAAGATCAGACAGAGTAAAGTCTCAACAAAAGAGTCAACAAAGATAGTCCCTA 720  
Db 661 TCCAAGATCAGACAGAGTAAAGTCTCAACAAAAGAGTCAACAAAGATAGTCCCTA 720  
QY 721 ATATCGGATCTAGACCGTGGTGTAGGGGTCAATCAGGAGGATAAGCATATCTGACCA 780  
Db 721 ACATCGGATCTAGACCGGGTCAATCAGGAGGATAAGCATATCTGACCA 780  
QY 781 TTGTAAACCTGGAGATATCTTAATGATAACAGTAAATGGCAACTTAGTTGACCGCGG 840  
Db 781 TTGTAAACCTGGAGATATCTTAATGATAACAGTAAATGGCAACTTAGTTGACCGCGG 840  
QY 841 GATATTTTAAATTTGAAAACAGGAAAAGCTCTGTATGAGATCAGATGCACCATAGACA 900  
Db 841 GATATTTTAAATTTGAAAACAGGAAAAGCTCTGTATGAGATCAGATGCACCATAGACA 900  
QY 901 TTGTGTGCTGAATGTATTACCAAAATGGAAGCATCCCAACGACAAACCAATTTCAAA 960  
Db 901 TTGTGTGCTGAATGTATTACCAAAATGGAAGCATCCCAACGACAAACCAATTTCAAA 960  
QY 961 ATGTGAACAAAGTTACATATGGAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020  
Db 961 ATGTGAACAAAGTTACATATGGAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020  
QY 1021 TGCCCACTGGATGAGGATATACCAAGCAAGCAATCAGA 1061  
Db 1021 TGCCCACTGGATGAGGATATACCAAGCAAGCAATCAGA 1061

RESULT 6  
US-09-762-861B-7  
; Sequence 7, Application US/09762861B  
; Patent No. 6579528  
; GENERAL INFORMATION:  
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher  
; APPLICANT: Education  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)  
; CURRENT APPLICATION NUMBER: US/09762,861B  
; CURRENT FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 1762  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (30)..(1724)  
; OTHER INFORMATION:  
US-09-762-861B-7

Query Match 97.3%; Score 1032.2; DB 4; Length 1762;  
Best Local Similarity 98.3%; Pred. No. 1.1e-302;  
Matches 1043; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
QY 1 AGCAAAAGCAGGGATATTTCTGTCAATCATGAGACAAACATTTTGTACTACTGA 60  
Db 1 AGCAAAAGCAGGGATATTTCTGTCAATCATGAGACAAACATTTTGTACTACTGA 60

QY 61 CCCATTGGGTCTCAGTCAAAACCCAGTGGAAACAAACACAGCCACATTTATGTCTGG 120  
Db 61 CCCATTGGGTCTCAGTCAAAACCCAGTGGAAACAAACACAGCCACATTTATGTCTGG 120  
QY 121 GACACCATGCAAGTACCAAAATGGAACATTTGGTAAACAAATTAATCTGATGACCAATTTGAGG 180  
Db 121 GACACCATGCAAGTACCAAAATGGAACATTTGGTAAACAAATTAATCTGATGACCAATTTGAGG 180  
QY 181 TGACAAATGCTTACTGAAATTTAGTTCAGAGCATTTCAATAGGGAATAATGCAACAACTCAT 240  
Db 181 TGACAAATGCTTACTGAAATTTAGTTCAGAGCATTTCAATAGGGAATAATGCAACAACTCAT 240  
QY 241 ATAAAGTTCTAGATGGAAGAAATTTGCAATTAATAGATGCAATGCTAGGAGACCCCACT 300  
Db 241 ATAGAGTTCTAGATGGAAGAAATTTGCAATTAATAGATGCAATGCTAGGAGACCCCACT 300  
QY 301 GTGATGCTTCCAGTATGAGAAATTTGGGACCTCTTCATAGAAAGAGCAGCGCTTTTCAGCA 360  
Db 301 GTGATGCTTCCAGTATGAGAAATTTGGGACCTCTTCATAGAAAGAGCAGCGCTTTTCAGCA 360  
QY 361 ATTGCTATCCCATATGACATCCCTGACTATGATCGCTCCGTTCCATTTGTAGCATCTCTCAG 420  
Db 361 GTTGTCTATCCCATATGACATCCCTGACTATGATCGCTCCGTTCCATTTGTAGCATCTCTCAG 420  
QY 421 GAAACATTTAGAAATTTCAACAGCAGAGGATTTCAATGAGCAGAGTGTCACTCAAAACGGAAGAA 480  
Db 421 GAAACATTTAGAAATTTCAACAGCAGAGGATTTCAATGAGCAGAGTGTCACTCAAAACGGAAGAA 480  
QY 481 GTGGAGCTTGCMAAAGGGGATCAGCGGATAGTTCTTTTAGCCGACTGAATTTGGCTTAACAA 540  
Db 481 GTGGAGCTTGCMAAAGGGGATCAGCGGATAGTTCTTTTAGCCGACTGAATTTGGCTTAACAA 540  
QY 541 AATCTGGAACCTCTTACCCCACTTGAATGTGACAAATGCTTAACTAAATAAATTTTCGACA 600  
Db 541 AATCTGGAACCTCTTACCCCACTTGAATGTGACAAATGCTTAACTAAATAAATTTTCGACA 600  
QY 601 AACTATACATCTGGGGATTTCAACCCGAGCTCAACCAAGAGCAGACAAATTTGTACA 660  
Db 601 AACTATACATCTGGGGATTTCAACCCGAGCTCAACCAAGAGCAGACAAATTTGTACA 660  
QY 661 TCCAAGATCAGGAGTAAAGTCTCAACAAAAGAGTCAACAAAGATAGTCCCTA 720  
Db 661 TCCAAGATCAGGAGTAAAGTCTCAACAAAAGAGTCAACAAAGATAGTCCCTA 720  
QY 721 ATATCGGATCTAGACCGTGGTGTAGGGGTCAATCAGGAGGATAAGCATATCTGACCA 780  
Db 721 ACATCGGATCTAGACCGGGTGAGGGGTCAATCAGGAGGATAAGCATATCTGACCA 780  
QY 781 TTGTAAACCTGGAGATATCTTAATGATAACAGTAAATGGCAACTTAGTTGACCGCGG 840  
Db 781 TTGTAAACCTGGAGATATCTTAATGATAACAGTAAATGGCAACTTAGTTGACCGCGG 840  
QY 841 GATATTTTAAATTTGAAAACAGGAAAAGCTCTGTATGAGATCAGATGCACCATAGACA 900  
Db 841 GATATTTTAAATTTGAAAACAGGAAAAGCTCTGTATGAGATCAGATGCACCATAGACA 900  
QY 901 TTGTGTGCTGAATGTATTACCAAAATGGAAGCATCCCAACGACAAACCAATTTCAAA 960  
Db 901 TTGTGTGCTGAATGTATTACCAAAATGGAAGCATCCCAACGACAAACCAATTTCAAA 960  
QY 961 ATGTGAACAAAGTTACATATGGAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020  
Db 961 ATGTGAACAAAGTTACATATGGAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020  
QY 1021 TGCCCACTGGATGAGGATATACCAAGCAAGCAATCAGA 1061  
Db 1021 TGCCCACTGGATGAGGATATACCAAGCAAGCAATCAGA 1061

RESULT 7  
US-10-065-133A-7  
; Sequence 7, Application US/10065133A  
; Patent No. 6685946

Query Match 97.4%; Score 1033.8; DB 4; Length 1762;  
Best Local Similarity 98.4%; Pred. No. 3.6e-303;  
Matches 1044; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 AGCAAAAGCAGGGGATATTTCTGTCATCATGAGACCAACCAATTTATTTGATACCTACTGA 60  
DB 1 AGCAAAAGCAGGGGATATTTCTGTCATCATGAGACCAACCAATTTATTTGATACCTACTGA 60

QY 61 CCATTGGTCTACAGTCAAAACCAACCCAGTGGAAACCAACACGACCACTATTTCTGCG 120  
DB 61 CCATTGGTCTACAGTCAAAACCAACCCAGTGGAAACCAACACGACCACTATTTCTGCG 120

QY 121 GACACATGTCAGTACCAATGGAACATTTGGTAAACCAATTAATCTGATGACCAAAATTTGAGG 180  
DB 121 GACACATGTCAGTACCAATGGAACATTTGGTAAACCAATTAATCTGATGACCAAAATTTGAGG 180

QY 181 TGACAAATGCTACTGAATTTAGTTCAGAGCAATTTCAATAGGGAATATGCAACAACTAT 240  
DB 181 TGACAAATGCTACTGAATTTAGTTCAGAGCAATTTCAATAGGGAATATGCAACAACTAT 240

QY 241 ATAAAGTTCTAGATGCAAGAAATTCACATTAATAGATGCAATGCTAGGAGACCCCACT 300  
DB 241 ATAGAGTTCTAGATGCAAGAAATTCACATTAATAGATGCAATGCTAGGAGACCCCACT 300

QY 301 GTGATGCTCTCCAGTATGAGAAATTTGGGACCTCTTTCATAGAAAGAGCAGCGCTTTTCAGCA 360  
DB 301 GTGATGCTCTCCAGTATGAGAAATTTGGGACCTCTTTCATAGAAAGAGCAGCGCTTTTCAGCA 360

QY 361 ATTGCTACCATATGACATCCCTGACTATGATCGTCCGTCATTTGATGATCCTCAG 420  
DB 361 GTTGTCTACCATATGACATCCCTGACTATGATCGTCCGTCATTTGATGATCCTCAG 420

QY 421 GAACATTAGAAATTCACAGCAGAGGATTCACATGACAGCTGCTCAATCAAAACGGAAGA 480  
DB 421 GAACATTAGAAATTCACAGCAGAGGATTCACATGACAGCTGCTCAATCAAAACGGAAGA 480

QY 481 GTGGAGCCTGCAAAAGGGGATCAGCGGATAGTTCTTTAGCCGACTGAATTTGGCTAAACA 540  
DB 481 GTGGATCTGCAAAAGGGGATCAGCGGATAGTTCTTTAGCCGACTGAATTTGGCTAAACA 540

QY 541 AATCTGGAACCTTTACCCCAATTTGAATGTGACAAATGCTTAAACAAATTTTCGACA 600  
DB 541 AATCTGGAACCTTTACCCCAATTTGAATGTGACAAATGCTTAAACAAATTTTCGACA 600

QY 601 AACTATACATCTGGGGATTTCAATCCCGAGCTCAACCAACAGCAGACAGAAATTTGTACA 660  
DB 601 AACTATACATCTGGGGATTTCAATCCCGAGCTCAACCAACAGCAGACAGAAATTTGTACA 660

QY 661 TCCAAAGAAATCAGGACGAGTAAACAGTCTCAACAAAGAAAGTCAACAAACAAATTAATCCCTTA 720  
DB 661 TCCAAAGAAATCAGGACGAGTAAACAGTCTCAACAAAGAAAGTCAACAAACAAATTAATCCCTTA 720

QY 721 ATATCGGATCTAGACGCTGGGTTAGGGTCAATTCAGGCAAGGATAGCATATCTGACCA 780  
DB 721 ACATCGGATCTAGACGCTGGGTTAGGGTCAATTCAGGCAAGGATAGCATATCTGACCA 780

QY 781 TTGTAAACCTGAGATATCTTAATGATAAACAAGTAAATGSCAACTTAGTTGACCCGCGG 840  
DB 781 TTGTAAACCTGAGATATCTTAATGATAAACAAGTAAATGSCAACTTAGTTGACCCGCGG 840

QY 841 GATATTTTAAATTTGAAAACAGGGAAAGCTCTGTAATGAGATCAGATGCAACCCATAGACA 900  
DB 841 GATATTTTAAATTTGAAAACAGGGAAAGCTCTGTAATGAGATCAGATGCAACCCATAGACA 900

QY 901 TTGTGTGCTGAATGATTAACCAATGGAAGCATTCCTCAACGACAAACCAATTTTCAA 960  
DB 901 TTGTGTGCTGAATGATTAACCAATGGAAGCATTCCTCAACGACAAACCAATTTTCAA 960

QY 961 ATGTGAACAAAGTTACATATGGAATGCCCAAGTATATCAGGCAAAACACCTTTAAAGC 1020  
DB 961 ATGTGAACAAAGTTACATATGGAATGCCCAAGTATATCAGGCAAAACACCTTTAAAGC 1020

QY 1021 TGGCCACTGGGATGAGGAATATACCAAAAAGCAAAATCAGA 1061  
DB 1021 TGGCCACTGGGATGAGGAATATACCAAAAAGCAAAATCAGA 1061

## RESULT 5

US-09-506-286B-7  
; Sequence 7, Application US/09506286B  
; Patent No. 6482414  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Younger, Julius S.  
; TITLE OF INVENTION: The University of Pittsburgh, of the Commonwealth  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EO-1-C2  
; CURRENT APPLICATION NUMBER: US/09/506,286B  
; PRIORITY FILING DATE: 2000-02-16  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/18593  
; PRIOR FILING DATE: 1999-08-12  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 1762  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (30)..(1724)  
US-09-506-286B-7

## Query Match 97.3%; Score 1032.2; DB 4; Length 1762;

Best Local Similarity 98.3%; Pred. No. 1.1e-302;  
Matches 1043; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 AGCAAAAGCAGGGGATATTTCTGTCATCATGAGACCAACCAATTTATTTGATACCTACTGA 60  
DB 1 AGCAAAAGCAGGGGATATTTCTGTCATCATGAGACCAACCAATTTATTTGATACCTACTGA 60

QY 61 CCCATTGGTCTACAGTCAAAACCAACCCAGTGGAAACCAACACGACCACTATTTCTGCG 120  
DB 61 CCCATTGGTCTACAGTCAAAACCAACCCAGTGGAAACCAACACGACCACTATTTCTGCG 120

QY 121 GACACATGTCAGTACCAATGGAACATTTGGTAAACCAATTAATCTGATGACCAAAATTTGAGG 180  
DB 121 GACACATGTCAGTACCAATGGAACATTTGGTAAACCAATTAATCTGATGACCAAAATTTGAGG 180

QY 181 TGACAAATGCTACTGAATTTAGTTCAGAGCAATTTCAATAGGGAATATGCAACAACTAT 240  
DB 181 TGACAAATGCTACTGAATTTAGTTCAGAGCAATTTCAATAGGGAATATGCAACAACTAT 240

QY 241 ATAAAGTTCTAGATGGAAGAAATTTGCAATTAATAGATGCAATGCTAGGAGACCCCACT 300  
DB 241 ATAGAGTTCTAGATGGAAGAAATTTGCAATTAATAGATGCAATGCTAGGAGACCCCACT 300

QY 301 GTGATGCTCTCCAGTATGAGAAATTTGGGACCTCTTTCATAGAAAGAGCAGCGCTTTTCAGCA 360  
DB 301 GTGATGCTCTCCAGTATGAGAAATTTGGGACCTCTTTCATAGAAAGAGCAGCGCTTTTCAGCA 360

QY 361 ATTTGCTACCATATGACATCCCTGACTATGATCGTCCGTCATTTGATGATCCTCAG 420  
DB 361 GTTGTCTACCATATGACATCCCTGACTATGATCGTCCGTCATTTGATGATCCTCAG 420

QY 421 GAACATTAGAAATTCACAGCAGAGGATTCACATGACAGCTGCTCAATCAAAACGGAAGA 480  
DB 421 GAACATTAGAAATTCACAGCAGAGGATTCACATGACAGCTGCTCAATCAAAACGGAAGA 480

QY 481 GTGGAGCCTGCAAAAGGGGATCAGCGGATAGTTCTTTAGCCGACTGAATTTGGCTAAACA 540  
DB 481 GTGGATCTGCAAAAGGGGATCAGCGGATAGTTCTTTAGCCGACTGAATTTGGCTAAACA 540

QY 541 AATCTGGAACCTTTTACCCCAATTTGAATGTGACAAATGCTTAAACAAATTTTCGACA 600

```
QY 901 TTGTGTGCTGAATGATATACCAAAATGGAAGCATCCCAACGACAAACCAATTCAAA 960
Db 901 TTGTGTGCTGAATGATATACCAAAATGGAAGCATCCCAACGACAAACCAATTCAAA 960
QY 961 ATGTGAACAAAGTTACATATGGAATAATGCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
Db 961 ATGTGAACAAAGTTACATATGGAATAATGCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
QY 1021 TGCCCACTGGGATGAGGAATATACCAAGAAAGCAAAATCAGA 1061
Db 1021 TGCCCACTGGGATGAGGAATATACCAAGAAAGCAAAATCAGA 1061

RESULT 3
US-10-065-133A-10
; Sequence 10, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (30)..(1724)
; OTHER INFORMATION:
US-10-065-133A-10

Query Match 97.4%; Score 1033.8; DB 4; Length 1762;
Best Local Similarity 98.4%; Pred. No. 3.6e-303;
Matches 1044; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGTAAGACCAACCATTTATTTGATACTACTGA 60
Db 1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGTAAGACCAACCATTTATTTGATACTACTGA 60
QY 61 CCCATTGGGTCTACAGTCAAAACCCCAACCAAGTGGAAACCAACACAGCCACATTTATGTCTGG 120
Db 61 CCCATTGGGTCTACAGTCAAAACCCCAACCAAGTGGAAACCAACACAGCCACATTTATGTCTGG 120
QY 121 GACACCATGCAAGTAGCAAAATGGAACATTTGGTAAAAACAATACTGATGACCAAAATTTGAGG 180
Db 121 GACACCATGCAAGTAGCAAAATGGAACATTTGGTAAAAACAATACTGATGACCAAAATTTGAGG 180
QY 181 TGCAAAATGCTACTGAATTTAGTTAGTTCAGAGCAATTTCAATAGGGAATAATGCAAACTCAT 240
Db 181 TGCAAAATGCTACTGAATTTAGTTAGTTCAGAGCAATTTCAATAGGGAATAATGCAAACTCAT 240
QY 241 ATAAAGTTCTAGATGGAAGAAATGCAATTAATAGATGCAATGCAATGCTAGGAGAGCCCCCACT 300
Db 241 ATAGAGTTCTAGATGGAAGAAATGCAATTAATAGATGCAATGCAATGCTAGGAGAGCCCCCACT 300
QY 301 GTGATGCTTCCAGATATGAGAAATGGGACCTCTTCATAGAAAGACGAGCGCTTTTCAGCA 360
Db 301 GTGATGCTTCCAGATATGAGAAATGGGACCTCTTCATAGAAAGACGAGCGCTTTTCAGCA 360
QY 361 ATTGCTACCCATATGACATCCCTGACTATGCTATGCTCGGTCCGATTTAGTATGCTCTCAG 420
Db 361 GTTGCTACCCATATGACATCCCTGACTATGCTATGCTCGGTCCGATTTAGTATGCTCTCAG 420
```

```
QY 421 GAACATTAGAATTACAGCAGAGGGAATTCATATGACAGAGTGTCTCACTCAAAACCGAAGAA 480
Db 421 GAACATTAGAATTACAGCAGAGGGAATTCATATGACAGAGTGTCTCACTCAAAACCGAAGAA 480
QY 481 GTGAGGCTGCAAAAGGGGATCAGCGGATAGTTCTTTTAGCGGACTGAATTTGGCTTAACAA 540
Db 481 GTGAGGCTGCAAAAGGGGATCAGCGGATAGTTCTTTTAGCGGACTGAATTTGGCTTAACAG 540
QY 541 AATCTGGAACACTTTACCCCACTTTGAATGTGACAAATGCCCTAACAAATAAATTTTCGACA 600
Db 541 AATCTGGAACACTTTACCCCACTTTGAATGTGACAAATGCCCTAACAAATAAATTTTCGACA 600
QY 601 AACTATACATCTGGGGGATTCATCACCCGAGCTCAAAACCAACAGCAGACAGAAATTTGTACA 660
Db 601 AACTATACATCTGGGGGATTCATCACCCGAGCTCAAAACCAACAGCAGACAGAAATTTGTACA 660
QY 661 TCCAAAGATCAGGACGAGTAACAGTCTCAACAAAAAGAAAGTCAACAAACGATAGTCCCTTA 720
Db 661 TCCAAAGATCAGGACGAGTAACAGTCTCAACAAAAAGAAAGTCAACAAACGATAGTCCCTTA 720
QY 721 ATATCGGATCTAGACCGGTGGGTAGGGGTCAATCAGGCGAGGATAGCATATATCTGACCA 780
Db 721 ATATCGGATCTAGACCGGTGGGTAGGGGTCAATCAGGCGAGGATAGCATATATCTGACCA 780
QY 781 TTGTAAAAACCTGGAGATATCTTAATGATAAACAAGTAATGGCAACTTAGTTGACCGCGGG 840
Db 781 TTGTAAAAACCTGGAGATATCTTAATGATAAACAAGTAATGGCAACTTAGTTGACCGCGGG 840
QY 841 GATATTTAAATTTGAAAAACAGGAAAGCTCTGTAATGAGATCAGATGATGATGATGATGAT 900
Db 841 GATATTTAAATTTGAAAAACAGGAAAGCTCTGTAATGAGATCAGATGATGATGATGATGAT 900
QY 901 TTTGTGTGCTGTAATGATTTACCAAAATGGAAGCATCCCAACGACAAACCAATTTCAAA 960
Db 901 TTTGTGTGCTGTAATGATTTACCAAAATGGAAGCATCCCAACGACAAACCAATTTCAAA 960
QY 961 ATGTGAACAAAGTTACATATGGAATAATGCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
Db 961 ATGTGAACAAAGTTACATATGGAATAATGCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
QY 1021 TGCCCACTGGGATGAGGAATATACCAAGAAAGCAAAATCAGA 1061
Db 1021 TGCCCACTGGGATGAGGAATATACCAAGAAAGCAAAATCAGA 1061

RESULT 4
US-10-434-811A-10
; Sequence 10, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (30)..(1724)
; OTHER INFORMATION:
US-10-434-811A-10
```



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 03:20:06 ; Search time 219 Seconds  
(without alignments)  
7927.350 Million cell updates/sec

Title: US-10-826-929A-1  
Perfect score: 1061  
Sequence: 1 agcaaaagcagggtatatt.....taccagaaagcaaatcaga 1061

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*

1: /cgn2\_6/ptodata/1/ina/5A COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCRU COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfileseq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1033.8	97.4	1762	US-09-506-286B-10	Sequence 10, Appl
2	1033.8	97.4	1762	US-09-762-861B-10	Sequence 10, Appl
3	1033.8	97.4	1762	US-10-065-133A-10	Sequence 10, Appl
4	1033.8	97.4	1762	US-10-434-811A-10	Sequence 10, Appl
5	1032.2	97.3	1762	US-09-506-286B-7	Sequence 7, Appli
6	1032.2	97.3	1762	US-09-762-861B-7	Sequence 7, Appli
7	1032.2	97.3	1762	US-10-065-133A-7	Sequence 7, Appli
8	1032.2	97.3	1762	US-10-434-811A-7	Sequence 7, Appli
9	1019.2	96.1	1698	US-09-622-951-1	Sequence 1, Appli
10	1018.4	96.0	1762	US-08-105-483-300	Sequence 300, App
11	1018.4	96.0	1762	US-08-709-209-300	Sequence 300, App
12	1018.4	96.0	1762	US-08-458-101-300	Sequence 300, App
13	1004.8	94.7	1695	US-09-506-286B-12	Sequence 12, Appl
14	1004.8	94.7	1695	US-09-762-861B-12	Sequence 12, Appl
15	1004.8	94.7	1695	US-10-065-133A-12	Sequence 12, Appl
16	1004.8	94.7	1695	US-10-434-811A-12	Sequence 12, Appl
17	1003.2	94.6	1695	US-09-506-286B-9	Sequence 9, Appli
18	1003.2	94.6	1695	US-09-762-861B-9	Sequence 9, Appli
19	1003.2	94.6	1695	US-10-065-133A-9	Sequence 9, Appli
20	1003.2	94.6	1695	US-10-434-811A-9	Sequence 9, Appli
21	976.2	92.0	1762	US-08-105-483-284	Sequence 284, App
22	976.2	92.0	1762	US-08-709-209-284	Sequence 284, App
23	976.2	92.0	1762	US-08-458-101-284	Sequence 284, App
24	947.2	89.3	1698	US-09-232-478-15	Sequence 15, Appl
25	947.2	89.3	1698	US-09-785-055-15	Sequence 15, Appl
26	607.2	57.2	1777	US-08-229-781-54	Sequence 54, Appl
27	607.2	57.2	1777	US-08-630-918-54	Sequence 54, Appl

28 607.2 57.2 1777 3 US-09-004-422-54 Sequence 54, Appl  
29 607.2 57.2 1777 4 US-09-918-568-54 Sequence 54, Appl  
30 549.2 51.8 1793 2 US-08-453-848-6 Sequence 6, Appli  
31 549.2 51.8 1793 3 US-09-169-027-6 Sequence 6, Appli  
32 544.4 51.3 1757 2 US-08-453-848-14 Sequence 14, Appl  
33 544.4 51.3 1757 3 US-09-169-027-14 Sequence 14, Appl  
34 541.2 51.0 1701 3 US-09-232-468A-21 Sequence 21, Appl  
35 541.2 51.0 1701 4 US-09-784-984B-17 Sequence 17, Appl  
36 541.2 51.0 1757 2 US-08-453-848-20 Sequence 20, Appl  
37 541.2 51.0 1757 3 US-09-169-027-20 Sequence 20, Appl  
38 148.2 14.0 1759 1 US-08-105-483-279 Sequence 279, App  
39 148.2 14.0 1759 1 US-08-709-209-279 Sequence 279, App  
40 148.2 14.0 1759 1 US-08-458-101-279 Sequence 279, App  
41 127.2 12.0 1721 3 US-08-686-968C-226 Sequence 226, App  
42 122.4 11.5 1110 1 US-08-229-781-57 Sequence 57, Appl  
43 122.4 11.5 1110 1 US-08-630-918-57 Sequence 57, Appl  
44 122.4 11.5 1110 3 US-09-004-422-57 Sequence 57, Appl  
45 122.4 11.5 1110 4 US-09-918-568-57 Sequence 57, Appl

ALIGNMENTS

RESULT 1  
US-09-506-286B-10  
; Sequence 10, Application US/09506286B  
; Patent No. 6482414  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2  
; CURRENT APPLICATION NUMBER: US/09/506,286B  
; PRIOR FILING DATE: 2000-02-16  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 1762  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (30)..(1724)  
US-09-506-286B-10

Query Match 97.4%; Score 1033.8; DB 4; Length 1762;  
Best Local Similarity 98.4%; Pred. No. 3.6e-303;  
Matches 1044; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 AGCAAAAGCAGGGGATATTTCTCAATCATGAGACCAACCAATTTTGTACTACTGA 60  
Db 1 AGCAAAAGCAGGGGATATTTCTCAATCATGAGACCAACCAATTTTGTACTACTGA 60

QY 61 CCATTGGGTCTACAGTCAAAACCCCAACCCAGTGGGCAACACACACATTATGTCTGG 120  
Db 61 CCATTGGGTCTACAGTCAAAACCCCAACCCAGTGGGCAACACACACATTATGTCTGG 120

QY 121 GACACCATGCTAGCAATGGAATGGTAAACATTAATGATGACCAATTTGAGG 180  
Db 121 GACACCATGCTAGCAATGGAATGGTAAACATTAATGATGACCAATTTGAGG 180

QY 181 TGACAAATGCTACTGAAATAGTTTCAGAGCATTTTCAATAGGAAATATGCAACATCAT 240  
Db 181 TGACAAATGCTACTGAAATAGTTTCAGAGCATTTTCAATAGGAAATATGCAACATCAT 240

QY 241 ATAAAGTTCTAGATGGAAGAAATTTGACATTAATAGATGCAATGCTAGAGACCCCACT 300  
Db 241 ATAGAGTTCTAGATGGAAGAAATTTGACATTAATAGATGCAATGCTAGAGACCCCACT 300

Page Blank (uspto)



```
Db 61 TCTGTGAGGTTCTCGCCCAAAACCTTCCAGGAAATGACAAACAGCAGCAACGCTGTGCC 120
Qy 118 TGGGACACCATGCTAGCAATGCAATGTTGTAACAACTACTGATGACCAAAATG 177
Db 121 TGGCAGCATATGATGTCGCAACGGAACGCTAGTGAACCAATACGAAATGATCAGATTG 180
Qy 178 AGGTGACAAATGCTACTGAAATAGTTCAGAGCATTTCAATAGGGAAATATGCAACAACT 237
Db 181 AAGTGACTAATGCTACTGAGCTGGTTCAAGGTTCTCAACAGGTAGATATGCGACATC 240
Qy 238 CATATAAGTTCTAGATGGAAGAAATGCAATTAATAGATCAATGCTAGGAGACCCCC 297
Db 241 CTCATCGAATCCTTGTATGGAAGAAATGCACTGATACATGCTCTATTGGGGAGCCCTC 300
Qy 298 ACTGTGATGCTCTTCCAGATGAGAAATGGGACCTCTCATAGAAAGAGCGCGCTTTCA 357
Db 301 ATGTGATGGCTTTCAAAATGAGAAATGGGACCTTTTGTGAACGCAAGCAAGCTTTCA 360
Qy 358 GCAATTTGCTACCATATGACATCCCTGACTATGATCGCTCCGGTCCATTTGTAGCATCCT 417
Db 361 GCAACTGTTTACCTTTATGATGCGCAGATTTATGCTCCCTTAGTCACTAGTTGCTCGT 420
Qy 418 CAGGAACATTAGAAATTCACAGCAGAGGATTCACATGAGCAGGTGTCTCAAAACGGA 477
Db 421 CAGGCACCTGAGTTTATCAATGAAGGCTTCAATTTGAGCTGGGCTCACTCAGAAATGGG 480
Qy 478 GAAGTGGAGCCTGCAAAAGGGGATCAGCGGATGTTCTTTAGCGAGCTGAATTTGGCTAA 537
Db 481 GAAGCTATGCTTGCAAAAGGGGACCTGATAACAGTTTCTTCACTAGTACGAACTGGTGT 540
Qy 538 CAATATCGGAACCTTTACCCCAATGGAATGTGACAAATGCTTAACCAATAAAATTTG 597
Db 541 ACAATCAGAAAGACATATCCAGTCTGACGTGACTATGCAACCAATGCAATTTG 600
Qy 598 ACAATCTATACATCTGGGGATTTATCAACCGAGTCAACCAACAGCAGACAGAAATGT 657
Db 601 ACAAACTGTACATTTGGGGAGTTCAACCCGAGCAGCAACCAAGCAAAACCAACTAT 660
Qy 658 ACATCCAGAAATCAGCAGAGTAACAGTCTCAACAAAGAGTCAACAAACGATAGTCC 717
Db 661 ATGTTCAAAGCATCAGGGAGTCAACAGTCTCCACCAAGAGAGCCAGCAAACTATAATCC 720
Qy 718 CTAATATCGGATCTAGACCGTGGGTAGGGTCAATCAGGAGGATAAGCATATACCTGA 777
Db 721 CGAATGTGGGTCTAGACCTGGTAAAGGGTCTGCTAGTAGAATAAGCATCTATTGA 780
Qy 778 CAATTTGTAACCTGAGATATCCTTAATGATAACAGTAATGGCAACTTAGTTGACCGC 837
Db 781 CAATAGTAACCCGGGAGACATCTGTTAATTAATAGCAACGGGAACCTAATTTGCTCCT 840
Qy 838 GGGGATATTTTAAATGAAACAGGAAAGAGTCTGTTAATGATGATGATGATGATGATGAT 897
Db 841 GGGGTTACTTCAAAATACGCACTGGGAAAGAGTCAATTAATGATGATGATGATGATGATG 900
Qy 898 ACATTTGTGTGTCTGAATGTATTAACCAATGGAAGCATCCCAACGACAAACCAATTC 957
Db 901 GCACCTGCAGTTCTGAATGATCATCTCAAAATGGAAGCATTCCTCAATGCAAGCCCTTTC 960
Qy 958 AAAATGTGACAAAGTTACATATGAAATGCCCCCAAGTATATCAGGCAAAACACTTTAA 1017
Db 961 AAAACGTAAACAAAGATCATATATGGGATGTTCCCAAGTATGTTTAAGCAAAACACTCTGA 1020
Qy 1018 AGCTGGCACTGGGATGAGGAATATACCAAGAAAGCAAAATCAGA 1061
Db 1021 AGTTGGCAACAGGATGCGGAATGTATCCAGAAACAAACTAGA 1064
```

RESULT 15  
ID ABQ82724  
XX ABQ82724 standard; cDNA; 1091 BP.  
AC ABQ82724;

```
XX 07-JAN-2003 (first entry)
DT Influenza A virus (A/Bangkok/1/79) haemagglutinin partial cDNA.
XX Influenza A virus; pathogenicity; RNA viral disease;
DE Influenza A virus; pathogenicity; RNA viral disease;
KW viral infection; selenium; vaccine; virucide; anti-HIV; gene; ss.
KW Influenza A virus.
OS
XX
XX Location/Qualifiers
FH 1..1091
FT /*tag= a
FT /partial
FT /product= "haemagglutinin protein"
XX
XX WO200278717-A2.
XX
XX 10-OCT-2002.
XX
XX 26-MAR-2002; 2002WO-EP003025.
XX
XX 28-MAR-2001; 2001US-00819387.
XX
XX (NEST ) SOC PROD NESTLE SA.
XX (UYNC-) UNIV NORTH CAROLINA.
XX
XX Beck M, German B, Levander O, Van Dael P;
XX WPI; 2002-759948/82.
XX P-PSDB; ABP53895.
XX
XX Treatment of influenza or reducing the risk of contracting influenza
XX involves administering selenium to an individual.
XX
XX Example 1; Page; 31pp; English.
XX
XX The present invention describes a method for treating influenza or
XX reducing the risk of contracting influenza, which involves administering
XX selenium to an individual. Also described is a method for enhancing the
XX efficacy of a viral vaccine by administering an antioxidant, preferably
XX selenium, to an individual receiving the viral vaccine. The method can be
XX used for treating influenza, for reducing the risk of contracting
XX influenza, and for enhancing the efficacy of viral vaccine (preferably
XX influenza vaccine) in an infant, elderly, a patient or a pet. It can also
XX be used for treating virus such as coxsackie and HIV virus. The method
XX provides an improved treatment for viral infection, by reducing in vivo
XX mutations of the RNA virus. The method also improves a vaccine used to
XX prevent transmission of an RNA viral disease. The present sequence
XX encodes the haemagglutinin protein from Influenza A virus.
XX (A/Bangkok/1/79). N.B. The present sequence is not given in the
XX specification, but is taken from the Genbank accession number AF201843,
XX as specified on page 7
```

```
Sequence 1091 BP; 345 A; 227 C; 255 G; 264 T; 0 U; 0 Other;
Query Match 53.4%; Score 566.2; DB 6; Length 1091;
Best Local Similarity 72.4%; Pred. No. 1.8e-149;
Matches 749; Conservative 0; Mismatches 283; Indels 3; Gaps 1;
Qy 30 ATGAAGCAACCAATATTTTGGATCTACTGACCATTGGGTCTACAGTCAAAACCCCAACC 89
Db 1 ATGAAGCACTCATTTGCTTTGAGCTACATTTTATGTTCTGCTTTTCGTCCTCAAAACCTTCCC 60
Qy 90 ---AGTGGAAACACACAGCCACATTATGTTGGGACACCATGAGTACGAAATGGACAA 146
Db 61 GGAAATGACAAACACAGCAGCAACGCTGTGCTGGGACACCATGAGTCCAAACGGAACG 120
Qy 147 TTGGTAAACCAATAACTGATGACCAAAATTTGAGGTGCAAAATGCTACTGAAATAGTTAG 206
Db 121 CTAGTGAACCAACATCAAGATGATCAATTTGAAGTGAATGCTACTGAGCTGTTGTCAG 180
Qy 207 AGCATTTTCAATAGGGAATAATATGCAACACTCATATAAAGTTCTTAGATGGAAATTTGC 266
```





```

FT misc_feature 904..1734
FT /*tag= e
FT /product= "Stem region of C-terminal domain"
XX
XX PF621339-A2.
XX
XX 26-OCT-1994.
XX
XX 20-APR-1994; 94EP-00302819.
XX
XX 20-APR-1993; 93JP-00115216.
XX
XX 16-MAR-1994; 94JP-00070194.
XX
XX (TAKI ) TAKARA SHUZO CO LTD.
XX
XX Okuno Y, Isegawa Y, Sasao F, Ueda S;
XX WPI; 1994-325949/41.
XX P-PSDB; AAH63590.
XX
XX Human influenza-A virus haemagglutinin polypeptide(s) - useful in
XX influenza-A vaccine composition.
XX
XX Example 2; Page 54-58; 68pp; English.
XX
XX This sequence was amplified using the primer sequences given in AAQ72852-
XX 54 and represents a cDNA which encodes the full length hemagglutinin (HA)
XX gene of the H3N2 subtype of human influenza A virus, strain
XX A2/Aichi/2/68. The full length protein encoded by this amplified cDNA
XX contains two conserved regions, the A' region, TGMRN and the B region,
XX QINGKLN(L/V)IK. These regions are close to each other in the stem of
XX the HA molecule and they represent epitopes which are recognised by the
XX antibody C179. C179 binds to the stem region of the HA molecule and thus
XX inhibits the membrane fusion action of the HA molecule and neutralises
XX the virus. Polypeptide molecules which contain the conserved peptide
XX regions, A and B, esp. HA molecules lacking the globular head region (see
XX also AAQ72807), are antigenically equivalent to the stem region of the HA
XX molecule of influenza A virus. These artificial peptides may be used as
XX vaccines for prophylaxis of influenza A virus infection. (Updated on 25-
XX MAR-2003 to correct FN field.)
XX
XX Sequence 1777 BP; 565 A; 363 C; 420 G; 429 T; 0 U; 0 Other;
XX
XX Query Match 57.2%; Score 607.2; DB 2; Length 1777;
XX Best Local Similarity 74.0%; Pred. No. 5.6e-161;
XX Matches 784; Conservative 0; Mismatches 273; Indels 3; Gaps 1;
XX
XX 5 AAAGCGGGGATATTTCTGTCATATCATGAGACCAACCATATTTTGATACTACTGACCCA 64
XX 12 AAAGCAGGGGATATTTCTATTAATCATGAGACCATATTTGCTTTTGAGCTATATTTCTG 71
XX
XX 65 TTGGGTCTACAGTCAAAAC---CCAAACCGAGTGAAACACACAGCCACATTTATGCTGGG 121
XX 72 TCTGGTCTCGGCCACAGACCTTCAGAGAAATGACACAGCAGCAACGCTGTCCTGGG 131
XX
XX 122 ACACCATGCACTAGCAAAATGGAACTTTGTAATAAACAATCACTGATGACCAATTTGAGGT 181
XX 132 ACATCATGCGGTGCCAAACCGAACACTAGTGAACAAATCAGACATGATCAGATTGAAGT 191
XX
XX 182 GACAAATGCTACTGAATTTAGTTCAGAGCATTTCAATAGGAAATATGCAACACTCATAT 241
XX 192 GACTAATGCTTACTGAGCTAGTTCAGAGCTCTCAACGGGGGAAAATATGCAACAACTCTCA 251
XX
XX 242 TAAAGTTCTAGATGGAGAAATTCATTAATAGATGCAATCTAGGAGACCCCTCACTG 301
XX 252 TCGAATCTTTGATGGAATAGACTGCACATGATAGATGCTCTATTGGGGACCTCTATTG 311
XX
XX 302 TGATGCTCTCCAGTATGAGAAATTTGGGACCTCTTTATAGAAAGACGAGCGCTTTACGCAA 361
XX 312 TGATGTTTTTCAAAATGAGACATGGGACCTTTTCGTTGAACGACGAGCAAAAGCTTTACGCAA 371
XX
XX 362 TTGCTACCCATATGACATCCCTGACTATGATGCTCCGCTCCATTTGTAGCATCTCTCAGG 421
XX

```

```

Db 372 CTGTATACCCCTTTATGATGTGCCAGATTATGCTCCCTTAGTGTACTAGTTGCTCTGCTCAGG 431
Qy 422 AACATTAGAAATTCACAGCAGAGGGATTTCACATGGACAGTGTCTACTCAAAAACGGAGAAG 481
Db 432 CACTCTGGAGTTTATCACTGAGGGTTTCACCTTGGACTGGGTCTACTCAGATGGGGGAAG 491
Qy 482 TGGAGCCTGCAAAAAGGGGATCAGCCGATAGTCTTTTAGCCGACTGAATTTGGCTAACAAA 541
Db 492 CAATGCTTTGCAAAAAGGGGACCTGGTAGCGGTTTTTTTCAGTAGACTGAACCTGGTTGCCAA 551
Qy 542 ATCTGGAACCTTTTACCCACATTTGAATGTGACATGCTTACATATAAATAAATTTTCGACAA 601
Db 552 ATCAGGAAGCACAATATCCAGTCTGTAACGTGACTATGCCAAACAAATGACAATTTTGACAA 611
Qy 602 ACTATACATCTGGGGGATTCATCACCCGAGCTCAAAACCAACAGCAGACAGAAATTTTACAT 661
Db 612 ACTATACATTTGGGGGATTCACCCCGAGCAGCAGCAACCAAGACAAACCCAGCTCTATGT 671
Qy 662 CCAAGAAATCAGGAACGAGTAAACAGTCTCAACAAAAGAAAGTCAACAAACGATAGTCCCTAA 721
Db 672 TCAAGCATCAGGAGAGTCAAGTCTCTTACCCAGGAGAGCCAGCAAACTATAATCCCGAA 731
Qy 722 TATCGGATCTAGACCGTGGGTAGGGTCAATCAGGACAGGATAAGCATATATCTGACCAT 781
Db 732 TATCGGGTCCAGACCCCTGGGTAAGGGTCTGTCTAGTAGAATAGCATCTATTGGACAT 791
Qy 782 TGTAAAACCTCGAGATATCTTAATGATAAAGCAATGCGCAATTTAGTTGCACCGCGGG 841
Db 792 AGTTAAGCGGGAGAGCTACTGGTAAATTAATAGTAATGGAACTTAATCGCTCTCTCGGG 851
Qy 842 ATATTTTAAATTTGAAAACGAGGAAAGCTCTGTAAATGATGATCAGATGACCCCATGACAT 901
Db 852 TTAATTTCAAAATGCGCACTGGGAAAGCTCAATATATGAGTCAAGTGCATGACCTATTGTATC 911
Qy 902 TTGTGCTGCTGATGATTTATACCAAAATGGAGCATCCCCACGACAAACCAATTTTCAAAA 961
Db 912 CTGTATTTCTGAATGCATCACTCCAAATGGAGCAATCCCAGATGACAGCCCTTTTCAAAA 971
Qy 962 TGTGAACAAAGTTTACATATGGAATGCCCCCAAGTATATCAGGCAAAACACATTTAAAGCT 1021
Db 972 CGTAAACAAAGATCACATATGGAGCATGCCCAAGTATGTTAAGCAAAACACCCCTGAAGTT 1031
Qy 1022 GGCACCTGGGATGAGGAATATACCAAGAAAGCAAAATTCAGA 1061
Db 1032 GGCACAGGGATGCGGAATGTACCAAGAAACAAACTAGA 1071
XX
XX RESULT 12
XX ABA93937 standard; DNA; 1765 BP.
XX
XX ABA93937;
XX
XX 07-MAY-2002 (first entry)
XX
XX Influenza A/Udorn/72 (H3N2) Strain HA encoding DNA SEQ ID NO:7.
XX
XX Influenza A/Udorn/72 (H3N2) strain; Influenzavirus A; diagnosis;
XX Influenza A virus; genome; gene; ds.
XX
XX Influenzavirus A.
XX
XX Key Location/Qualifiers
XX CDS 30..1730
XX /*tag= a
XX /product= "HA protein"
XX
XX WO200200884-A2.
XX
XX 03-JAN-2002.
XX
XX 21-JUN-2001; 2001WO-US019826.
XX

```

FT CDS 1. .1698  
 FT /\*tag= a  
 FT /product= "haemagglutinin protein"  
 FN PR2751226-A1.  
 XX 23-JAN-1998.  
 XX 19-JUL-1996; 96FR-00009400.  
 XX 19-JUL-1996; 96FR-00009400.  
 XX (INNR ) RHONE MERIEUX SA.  
 XX Audonnet JCF, Bouchardon A, Riviere MEA;  
 XX WPI: 1998-112826/11.  
 XX P-PSDB; AAW44946.  
 XX Multi-valent polynucleotide vaccines against equine pathogens - consist  
 PT of at least 3 plasmids able to express protective antigens from specified  
 PT viruses.  
 XX Example 14; Fig 8; 49pp; French.  
 XX The invention relates to a multivalent vaccine for protecting horses  
 CC against several pathogens, especially pathogens associated with  
 CC respiratory and digestive diseases. The pathogens are especially selected  
 CC from equine herpesvirus (EHV), equine influenza virus (EIV), Clostridium  
 CC tetani, Borrelia burgdorferi, Eastern, Western or Venezuelan equine  
 CC encephalomyelitis viruses (EEEV, WEEV and VEEV, respectively) and rabies  
 CC virus. The vaccines are preferably composed of polynucleotide sequences  
 CC encoding 3 antigens, all as part of vectors. This sequence represents the  
 CC coding region of the EIV Fontainebleau strain haemagglutinin gene. The  
 CC sequence was subcloned into the plasmid pVR1012 to generate plasmid  
 CC pAB099 for use in the vaccine  
 XX Sequence 1698 BP; 604 A; 319 C; 384 G; 391 T; 0 U; 0 Other;  
 SQ  
 Query Match 89.3%; Score 947.2; DB 2; Length 1698;  
 Best Local Similarity 94.9%; Pred. No. 3.8e-53;  
 Matches 979; Conservative 0; Mismatches 53; Indels 0; Gaps 0;  
 QY 30 ATGAGACAAACCATTTATTTGATCTACTACTGACCCATGGGTCTACAGTCAAAACCCCAACC 89  
 DB 1 ATGAGACAAACCATTTATTTGATCTACTACTGACCCATGGGTCTACAGTCAAAACCCCAACC 60  
 QY 90 AGTGAACAACACAGCCACATTTATGCTCTGGGACACCATGCGATGAGCAAAATGGAAACATTG 149  
 DB 61 AGTGGCAACAACACAGCCACATTTATGCTCTGGGACACCATGCGATGAGCAAAATGGAAACATTG 120  
 QY 150 GTAAAAACAATACTGATGACCAATTCAGGTGACAAATGCTACTGAAATTTAGTTCAGAGC 209  
 DB 121 GTAAAAACAATACTGATGACCAATTCAGGTGACAAATGCTACTGAAATTTAGTTCAGAGC 180  
 QY 210 ATTTCAATAGGGAATATGCAACCACTCATATAAAGTTCTAGATGGAGAAATGGCACA 269  
 DB 181 ACTTCAATAGGGAATATGCAACCACTCATATAAAGTTCTAGATGGAGAAATGGCACA 240  
 QY 270 TTAATAGATGCAATGCTAGGAGACCCCACTGTGATGCTTCCAGTATGAGAAATGGGAC 329  
 DB 241 TTAATAGATGCAATGCTAGGAGATCCCACTGTGATGCTTCCAGTATGAGAAATGGGAC 300  
 QY 330 CTCCTTCATAGAAGAGAGCGCTTTCAGCAATTCCTACCAATGACATCCCTGACTAT 389  
 DB 301 CTCCTTCATAGAAGAGAGCGCTTTCAGCAATTCCTACCAATGACATCCCTGACTAT 360  
 QY 390 GCATCGCTCCCGTCCATTTAGTATCTCTCAGGAAACATTAGAAATTCACAGCAGAGGATTC 449  
 DB 361 GCATCGCTCCCGTCTATTGTGCACTTTCAGGAAACATTAGAAATTCACAGCAGAGGATTC 420  
 QY 450 ACATGGACAGGTGTCTCACTCAAAACCGGAAGAGTGGAGCTGCAAAAGGGGATTCAGCCGAT 509

Db 421 ACATGGACAGGTGTCACTCAAAACCGAAGAGTGGCGCTCTGACAGAGGGGATCAGCCGAT 480  
 QY 510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTCGAAACTCTTACCCACACATTGAAT 569  
 Db 481 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTCGAAACTCTTACCCACACATTGAAT 540  
 QY 570 GTGCAATGCTTAACAATAAAATTTTCGACAAAATCTATACATCTCTGGGGATTCATCACC 629  
 Db 541 GTAAACAATGCTTAACAATAAAATTTTCGATAAAATCTATACATCTCTGGGGATTCATCACC 600  
 QY 630 AGCTCAAAACCAACAGCAGACAGAAATTTGATGTCCTCAAGAAATTTAGGGCGAGTAACTCTCA 689  
 Db 601 AGCAAAACAATGATGAGCAGACAAAATTTGATGTCCTCAAGAAATTTAGGGCGAGTAACTCTCA 660  
 QY 690 ACAAAGAGAGTCAACAAAATTTGATGTCCTCAAGAAATTTAGGGCGAGTAACTCTCA 749  
 Db 661 ACAAAGAGAGTCAACAAAATTTGATGTCCTCAAGAAATTTAGGGCGAGTAACTCTCA 720  
 QY 750 CAATCAGCAGGATTAAGCATATTTCTGGACCAATTTGTAATCTCTGGAGATATCTTAATGATA 809  
 Db 721 CAATCAGCAGGATTAAGCATATTTCTGGACCAATTTGTAATCTCTGGAGATATCTTAATGATA 780  
 QY 810 AACAGTAATGCAACTTAGTTGACCGCGGGGATATTTTAAATTTGAAACAGGGAAGAC 869  
 Db 781 AACAGTAATGCAACTTAGTTGACCGCGGGGATATTTTAAATTTGAAACAGGGAAGAC 840  
 QY 870 TCTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 929  
 Db 841 TCTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
 QY 930 GGAAGCATGCCCAACGACCAACCAATTTTCAAAATGTGAACAAAGTTTACATATGGAATGTC 989  
 Db 901 GGAAGCATGCCCAACGACCAACCAATTTTCAAAATGTGAACAAAGTTTACATATGGAATGTC 960  
 QY 990 CCCAAGTATATCAGCAGCAAAACACATTTAAAGTGGCCACTGGGATGAGGAATATACCAGAA 1049  
 Db 961 CCCAAGTATATCAGCAGCAAAACATTTTGAAGTGGCCACTGGGATGAGGAATATACCAGAA 1020  
 QY 1050 AAGCAAAATCAGA 1061  
 Db 1021 AAGCAAAATCAGA 1032  
 RESULT 11  
 ID AAQ72855 standard; cDNA; 1777 BP.  
 AC AAQ72855;  
 XX 25-MAR-2003 (revised)  
 DT 23-JUN-1995 (first entry)  
 XX Full length H3N2 influenza A virus, strain A2/Aichi/2/68 HA gene.  
 DE Conserved peptide; stem region; hemagglutinin; HA; H1N1; H2N2; PCR;  
 KW subtype; human; influenza A virus; immunogenic artificial peptide;  
 KW antigen; vaccine; infection; polymerase chain reaction; primer; amplify;  
 KW C179; region A; region B; ds.  
 XX Influenza A virus.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 36..1737  
 FT /\*tag= a  
 FT /product= "Full length HA from H3N2 subtype"  
 FT sig\_peptide 37..84  
 FT /\*tag= b  
 FT misc\_feature 85..246  
 FT /\*tag= c  
 FT /product= "Stem region of N-terminal domain"  
 FT misc\_feature 247..903  
 FT /\*tag= d  
 FT /product= "Globular head domain"

DE EIV HA (A1/Fontainebleau/79).

XX Equine influenza virus; EIV; hemagglutinin; HA; A1/Fontainebleau/79;

KW expression cassette; NYVAC; ALVAC; recombinant vector;

KW polymerase chain reaction; PCR; vaccinia virus; H6 promoter;

KW canarypox virus; Copenhagen vaccine strain; virulence factor;

KW deletion loci; recipient loci; ss.

XX Synthetic.

OS

XX

XX W09215672-A1.

XX

XX 17-SEP-1992.

XX

XX 09-MAR-1992; 92WO-US001906.

XX

XX 07-MAR-1991; 91US-00666056.

PR 11-JUN-1991; 91US-00713967.

PR 06-MAR-1992; 92US-00847951.

XX

XX (VIRO-) VIROGENETICS CORP.

PA

XX Paoletti E, Perkus ME, Taylor J, Tartaglia J, Norton EK;

PI Riviere M, De Taisene C, Limbach KJ, Johnson GP, Pincus SE, Cox WI;

PI Francis J, Gettig RR;

XX WPI; 1992-331718/40.

XX

XX Vaccine comprises recombinant, attenuated pox-virus - use for vaccinating

PT against viral infections such as rabies, hepatitis B, HIV, HSV, EBV, CMV,

PT mumps etc.

XX

XX Disclosure; Fig 24; 456pp; English.

PS

XX

XX The sequence given encodes the equine influenza virus (EIV) hemagglutinin

CC (HA) (A1/Fontainebleau/79). This sequence was used to generate an

CC expression cassette for the insertion of the EIV HA gene into NYVAC and

CC ALVAC recombinant vectors. The HA gene sequence was isolated from an EIV

CC cDNA library and was amplified by polymerase chain reaction. The HA gene

CC sequence was fragmented and then reconstituted aligned with the vaccinia

CC virus H6 promoter. NYVAC is derived from a Copenhagen vaccine strain of

CC vaccinia virus and ALVAC is derived from a canarypox virus which has been

CC modified by deletion of non-essential regions of the genome encoding

CC known or potential virulence factors. The deletion loci of both vectors

CC were engineered as recipient loci for the insertion of foreign genes. See

CC also AAQ3591-864. (Updated on 25-MAR-2003 to correct FN field.)

XX

SQ Sequence 1762 BP; 626 A; 331 C; 395 G; 410 T; 0 U; 0 Other;

Query Match 92.0%; Score 976.2; DB 2; Length 1762;

Best Local Similarity 95.0%; Pred. No. 2.4e-265;

Matches 1008; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 AGCAAGAGCAGGGGATATTTCTGTCATCATGAGACCAACCATTTTGTACTACTGA 60

DB 1 AGCAAGAGCAGGGGATATTTCTGTCATCATGAGACCAACCATTTTGTACTACTGA 60

QY 61 CCATTTGGGTCTCAGTCAAAACCCACACAGTGGGAAACACACAGCCACATTTGTCTGG 120

DB 61 CCATTTGGGTCTCAGTCAAAACCCACACAGTGGGAAACACACAGCCACATTTGTCTGG 120

QY 121 GACACCATGAGTGGGAAATGGAACATTTGTAACCAATTAAGTGGGAAATTTGAGG 180

DB 121 GACACCATGAGTGGGAAATGGAACATTTGTAACCAATTAAGTGGGAAATTTGAGG 180

QY 181 TGCAAAATGCTACTGAAATTTAGTTCAGAGCATTTCAATAGGGAATAATGCAACACTCAT 240

DB 181 TGCAAAATGCTACTGAAATTTAGTTCAGAGCATTTCAATAGGGAATAATGCAACACTCAT 240

QY 241 ATAAAGTTCTAGATGGGAAATTTGACATTAATAGTGCATGCTAGGAGACCCCACT 300

DB 241 ATAGGGTTCTAGATGGGAAATTTGACATTAATAGTGCATGCTAGGAGATCCCACT 300

QY 301 GTGATGTTCTCCAGTATGAGAAATTTGGGACCTCTTTCATAGAAAGAGAGCGCTTTTCAGCA 360

DB 301 GTGATGTTCTCCAGTATGAGAAATTTGGGACCTCTTTCATAGAAAGAGAGCGCTTTTCAGCA 360

QY 361 ATTGCTACCATATGACATCCCTGACTATGATCGCTCCGCTCCATTTGTAGCATCTTCAG 420

DB 361 ATTGCTACCATATGACATCCCTGACTATGATCGCTCCGCTCCATTTGTAGCATCTTCAG 420

QY 421 GAACATTAGAATTCACAGCAGAGGGATTCACATGAGACAGGTGTCTACTCAAAACGGAAGAA 480

DB 421 GAACATTAGAATTCACAGCAGAGGGATTCACATGAGACAGGTGTCTACTCAAAACGGAAGAA 480

QY 481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTCTTTTAGCCGACTGAATTTGGCTTAAACAG 540

DB 481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTCTTTTAGCCGACTGAATTTGGCTTAAACAG 540

QY 541 AATCTGGAAATCTTTTACCCGACATTTGAATGTAACCAATGCTTAACCAATTAACCAATTTTCGATA 600

DB 541 AATCTGGAAATCTTTTACCCGACATTTGAATGTAACCAATGCTTAACCAATTAACCAATTTTCGATA 600

QY 601 AACTATACATCTGGGGGATTCATCACCAGCTCAAAACCAACAGCAGACAGAAATTTGTACA 660

DB 601 AACTATACATCTGGGGGATTCATCACCAGCTCAAAACCAACAGCAGACAGAAATTTGTACA 660

QY 661 TCCAAAGAATCAGGACGAGTAAACAGTCTCAACAAAAAGAGTCAACAAACCAATTAATCCCA 720

DB 661 TCCAAAGAATCAGGACGAGTAAACAGTCTCAACAAAAAGAGTCAACAAACCAATTAATCCCA 720

QY 721 ATATCGGATCTAGACCGTGGGTAGGGTCAATCAGGAGGATAGGATATATTTGACCA 780

DB 721 ATATCGGATCTAGACCGTGGGTAGGGTCAATCAGGAGGATAGGATATATTTGACCA 780

QY 781 TTGTAAAAACCTGGAGATATCCTTAATGATAAAGAGTAAATGGCAACTTAGTTGCACCGCGGG 840

DB 781 TTGTAAAAACCTGGAGATATCCTTAATGATAAAGAGTAAATGGCAACTTAGTTGCACCGCGGG 840

QY 841 GATATTTTAAATTTGAAAAACAGGAAAGTCTGTAAATGAGATCAGATGACCCCATAGACA 900

DB 841 GATATTTTAAATTTGAAAAACAGGAAAGTCTGTAAATGAGATCAGATGACCCCATAGACA 900

QY 901 TTTGTGTCTCAATGATTAACCAATGGAAGCATCCCAACGACAAACCATTTTCAAA 960

DB 901 TTTGTGTCTCAATGATTAACCAATGGAAGCATCCCAACGACAAACCATTTTCAAA 960

QY 961 ATGTGAAACAAAGTTACATATGGAATAATGCCCAAGTATATATCAGGCAAAACACTTTTAAAGC 1020

DB 961 ATGTGAAACAAAGTTACATATGGAATAATGCCCAAGTATATATCAGGCAAAACACTTTTAAAGC 1020

QY 1021 TGGCCACTGGGATGAGGAATATACAGAAAAAGCAAAATCAGA 1061

DB 1021 TGGCCACTGGGATGAGGAATATACAGAAAAAGCAAAATCAGA 1061

RESULT 10

AAV49391

ID AAV49391 standard; DNA; 1698 BP.

XX

XX AAV49391;

XX

XX 28-OCT-1998 (first entry)

XX

XX EIV Fontainebleau strain haemagglutinin gene.

XX

XX Multivalent vaccine; horse; pathogen; respiratory disease; EHV; EIV;

KW Clostridium tetani; Borrelia burgdorferi; equine influenza virus; EEEV;

KW Eastern equine encephalomyelitis virus; equine herpesvirus; EEEV; VEEV;

KW Western equine encephalomyelitis virus; digestive disease; rabies virus;

KW Venezuelan equine encephalomyelitis virus; vector; primer; PCR;

XX amplification; haemagglutinin; ss.

XX

OS Equine influenza virus.

XX

XX Location/Qualifiers

PH Key

Db 901 GGAAGCATCCCAACGACAAACCAATTCAAATGTGAACAAATTTACATATGGAATGC 960  
QY 990 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1049  
Db 961 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATGTACAGAA 1020  
QY 1050 AAGCAAAATCAGA 1061  
Db 1021 AAGCAAAATCAGA 1032

## RESULT 8

AAZ47007  
ID AAZ47007 standard; DNA; 1698 BP.

XX AAZ47007;

AC AAZ47007;

DT 29-FEB-2000 (first entry)

XX Equine influenza virus strain Newmarket 2/93 HA gene.

DE Antibacterial; antiviral; primer; RT-PCR; amplification; haemagglutinin;  
KW recombinant; vaccine; viral vector; pathogen; adjuvant; methacrylic acid;  
KW maleic anhydride; alkenyl derivative; animal; herpes virus; tetanus;  
KW influenza virus; feline leukemia; canine distemper; ss.

XX Equine influenza virus.

XX WO9944633-A1.

PN 10-SEP-1999.

PD 01-MAR-1999; 99WO-PR000453.

PF 03-MAR-1998; 98FR-00002800.

XX (MERI-) MERIAL.

PI Audonnet JF, Minke JM;

XX WPI; 2000-022918/02.

DR Live recombinant vaccine comprising viral vector and polymeric adjuvant,  
PT particularly directed against animal herpes and influenza viruses.

PS Example 5; Fig 1; 41pp; French.

CC This sequence represents the haemagglutinin (HA) gene from the equine  
CC influenza virus strain Newmarket 2/93. The gene was amplified and the  
CC product was used to generate a live recombinant vaccine which comprises:  
CC (1) a viral vector including, and expressing in vivo, a heterologous  
CC nucleotide sequence particularly a gene from a pathogen; and (2) at least  
CC one adjuvant, i.e. a (meth)acrylic acid polymer or a copolymer of maleic  
CC anhydride and alkenyl derivatives. The vaccines are used particularly to  
CC protect against animal herpes or influenza viruses, but also feline  
CC leukemia, tetanus and canine distemper

XX Sequence 1698 BP; 619 A; 312 C; 372 G; 395 T; 0 U; 0 Other;

SQ Query Match 92.7%; Score 984; DB 3; Length 1698;

Best Local Similarity 97.1%; Pred. No. 1.5e-267;

Matches 1002; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 30 ATGAGCAACCAATTTTGTATCTACTGACCCATTTGGGTCTACAGTCAAAACCCACACC 89

Db 1 ATGAGCAACCAATTTTGTATCTACTGACCCATTTGGGTCTACAGTCAAAACCCACACC 60

QY 90 AGTGGAAACAACACAGCCACATTTATGCTGGGACACCATGAGTAGCAAAATGGAAACATTG 149

Db 61 AGTGGCAACAACACAGCCACATTTATGCTGGGACACCATGAGTAGCAAAATGGAAACATTG 120

QY 150 GTAAAAACAATACTGATGACCAAAATTTGAGGTGACAAATGCTACTGTAATTAGTTACAGAC 209

Db 121 GTAAAAACAATACTGATGACCAAAATTTGAGGTGACAAATGCTACTGTAATTAGTTCCAGAC 180  
QY 210 ATTTCAATAGGAAAAATATGCAACAACTCATATAAAGTTCTAGATGGAGAAATTTGCACA 269  
Db 181 ATTTCAATAGGAAAAATATGCAACAACTCATATAAAGTTCTAGATGGAGAAATTTGCACA 240  
QY 270 TTAATAGATGCAATGCTAGGAGACCCCACTGTCATGCTCTCCAGTATGAGAAATTTGGAC 329  
Db 241 TTAATAGATGCAATGCTAGGAGACCCCACTGTCATGCTCTCCAGTATGAGAAATTTGGAC 300  
QY 330 CTCTTTATAGAAAGACAGCGCTTTTACGAAATTTGCTACCCATATGACATCCCTGACTAT 389  
Db 301 CTCTTTATAGAAAGACAGCGCTTTTACGAAATTTGCTACCCATATGACATCCCTGACTAT 360  
QY 390 GCATCGCTCCGTCCTATTTAGCATCTCTCAGGAACTATTAGAAATTTCAACAGAGAGGATTC 449  
Db 361 GCATCGCTCCGTCCTATTTAGCATCTCTCAGGAACTATTAGAAATTTCAACAGAGAGGATTC 420  
QY 450 ACATGGACAGGTGTCCTCAAAACGGAAGAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509  
Db 421 ACATGGACAGGTGTCCTCAAAACGGAAGAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 480  
QY 510 AGTTTCTTTAGCCGACTGAATTTGGCTAAACAAATCTTGAAACTCTTACCCACATTTGAAT 569  
Db 481 AGTTTCTTTAGCCGACTGAATTTGGCTAAACAAATCTTGAAACTCTTACCCACATTTGAAT 540  
QY 570 GTGCAATGCTTAACAATAAATTTTCGACAAACTATATACATCTGGGGGATTCATCACC 629  
Db 541 GTGCAATGCTTAACAATAAATTTTCGACAAACTATATACATCTGGGGGATTCATCACC 600  
QY 630 AGCTCAAAACCAACAGCAGACAGATTTGTACATCCAAAGATCAGGACGAGTAACTCTCA 689  
Db 601 AGCTCAAAACCAACAGCAGACAGATTTGTATATCCAGAAATCAGGACGAGTAACTCTCA 660  
QY 690 AAAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCTGGGTTAGGGGT 749  
Db 661 ACAGAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGGACGAGTAACTCTCA 720  
QY 750 CAATCAGCAGGATGAGCATATATCTGGACCATTTGTAAACCTGGAGATATCTTAATGATA 809  
Db 721 CAATCAGCAGGATGAGCATATATCTGGACCATTTGTAAACCTGGAGATATCTTAATGATA 780  
QY 810 AACAGTATGCAACTTAGTTTGACCCGCGGGATTTTAAATTTGAAACAGGGAAGAC 869  
Db 781 AACAGTATGCAACTTAGTTTGACCCGCGGGATTTTAAATTTGAGAACAGGGAAGAC 840  
QY 870 TCTGTAATGAGATCAGATGCACCCATAGACATTTTGTGTCTGTAATGTATTACCCAAAT 929  
Db 841 TCTGTAATGAGATCAGATGCACCTCATAGACATTTTGTGTCTGTAATGTATTACCCAAAT 900  
QY 930 GGAAGCATCCCAACGACAAACCAATTTCAAAATGTGAACAAAGTTACATATGGAAAAATGC 989  
Db 901 GGAAGCATCCCAACGACAAACCAATTTCAAAATGTGAACAAATTTACATATGGAAAAATGC 960  
QY 990 CCCAAGTATATCAGGCAAAACACTTTTAAAGCTGCCACTGGGATGAGGAATATATACAGAA 1049  
Db 961 CCCAAGTATATCAGGCAAAACACTTTTAAAGCTGCCACTGGGATGAGGAATGTATACAGAA 1020

## RESULT 9

AAQ29111

ID AAQ29111 standard; DNA; 1762 BP.

XX AC AAQ29111;

XX AC AAQ29111;

DT 25-MAR-2003 (revised)

XX 24-FEB-1993 (first entry)

QY 661 TCCAGAAATCAGACGAGTAACAGTCTCAACAAAAAGAGTCAACAAACGATAGTCCCTA 720  
DB 685 TCCAGAAATCAGGCGAGTAACAGTCTCAACAAAAAGAGTCAACAAACGATAGTCCCTA 744  
QY 721 ATATCGGATCTAGACCGTGGGTAGGGTCAATCAGGCGAGGATAAGCATATATCGGACCA 780  
DB 745 ACATCGGATCTAGACCGTGGGTAGGGTCAATCAGGCGAGGATAAGCATATATCGGACCA 804  
QY 781 TTGTAACCTGAGATATCTTAATGATTAACAGTAATGGCAACTAGTGTGACCGCGG 840  
DB 805 TTGTAACCTGAGATATCTTAATGATTAACAGTAATGGCAACTAGTGTGACCGCGG 864  
QY 841 GATATTTTAAATTTGAAACAGGAAAGCTCTGTAATGAGATCAGATGCAACCATAGACA 900  
DB 865 GATATTTTAAATTTGAAACAGGAAAGCTCTGTAATGAGATCAGATGCAACCATAGACA 924  
QY 901 TTTGTGTCTGCTGAATGATTAACCAAAATGGAAGCATCCCCAAGTATATCAGGCAACCATTTAAAGC 960  
DB 925 CTGTGTGTCTGCTGAATGATTAACCAAAATGGAAGCATCCCCAAGTATATCAGGCAACCATTTCAAA 984  
QY 961 ATGTGAACAAAGTTACATATGGAATGCAAAATGCAAAATGCAAAATGCAAAATGCAAA 1020  
DB 985 ATGTGAACAAAGTTACATATGGAATGCAAAATGCAAAATGCAAAATGCAAAATGCAAA 1044  
QY 1021 TGSCCACTGGGATGAGGAATATACCAAGAAAGCAAAATCAGA 1061  
DB 1045 TGSCCACTGGGATGAGGAATGCAAGGAAGCAAAATCAGA 1085

## RESULT 7

AZ30211  
ID AZ30211 standard; DNA; 1698 BP.  
XX AZ30211;  
XX  
DT 11-FEB-2000 (first entry)  
XX  
DE Sequence of the haemagglutinin (HA) gene of EIV strain Newmarket 2/93.  
XX  
KW Haemagglutinin gene; EIV; strain Newmarket 2/93; DNA vaccine; horse;  
KW acrylic acid polymer; methacrylic acid polymer; copolymer;  
KW maleic anhydride; alkenyl derivative; animal vaccine; viral infection;  
KW bacterial infection; ss.  
XX  
OS Equine influenza virus.  
XX  
PN FR2776928-A1.  
XX  
PD 08-OCT-1999.  
XX  
PF 03-APR-1998; 98PR-00004409.  
XX  
PR 03-APR-1998; 98PR-00004409.  
XX  
PA (MERI-) MERIAL SAS.  
XX  
PI Audonnet JCF, Minke JM;  
XX  
DR WPI; 1999-593389/51.  
XX  
PT Vaccine containing naked DNA and acrylic acid polymer or maleic anhydride  
PT copolymer, for protection against viral or bacterial diseases in animals.  
XX  
PS Example 8; Fig 1; 34pp; French.  
XX  
CC The present sequence represents the haemagglutinin gene of Equine  
CC influenza virus (EIV) strain Newmarket 2/93. The sequence was used to  
CC prepare a DNA vaccine for horses, representative of the DNA vaccines of  
CC the invention. The specification describes a DNA vaccine that comprises  
CC naked DNA encoding an antigenic polypeptide, and at least one adjuvant  
CC that is an acrylic or methacrylic acid polymer or a copolymer of maleic  
CC anhydride with an alkenyl derivative. The vaccines are simple and easy to

CC prepare (simply by mixing components) and they do not involve any strong  
CC interactions between DNA and other components that are likely to cause  
CC complex formation. The vaccines are used to protect animals (pigs,  
CC horses, dogs, cattle, cats or birds) against a wide variety of viral or  
CC bacterial infections

XX SQ Sequence 1698 BP; 619 A; 312 C; 372 G; 395 T; 0 U; 0 Other;

Query Match 92.7%; Score 984; DB 2; Length 1698;

Best Local Similarity 97.1%; Pred. No. 1.5e-267; Indels 0; Gaps 0;  
Matches 1002; Conservative 0; Mismatches 30;

QY 30 ATGAAGACAACCACTATTATTTGATCTACTGACCCCATCGGCTCAGTCAAAACCAACC 89  
DB 1 ATGAAGACAACCACTATTATTTGATCTACTGACCCCATCGGCTCAGTCAAAACCAACC 60  
QY 90 AGTGAACAACAACGACCACTATTATTTGATCTGTCGGACCACTGAGTCAAAATGGAACATG 149  
DB 61 AGTGAACAACAACGACCACTATTATTTGATCTGTCGGACCACTGAGTCAAAATGGAACATG 120  
QY 150 GTAAAAACAATAAATCTGATGACCAAAATTCAGGTGACAAATGCTACTGAAATTTAGTTCAGAGC 209  
DB 121 GTAAAAACAATAAATCTGATGACCAAAATTCAGGTGACAAATGCTACTGAAATTTAGTTCAGAGC 180  
QY 210 ATTTCAATAGGGAATAATATGCAACAACCTCATATATAAGTTCTAGATGGAAGAAATTCACACA 269  
DB 181 ATTTCAATAGGGAATAATATGCAACAACCTCATATATAAGTTCTAGATGGAAGAAATTCACACA 240  
QY 270 TTAATAGATCAATGCTAGGAGACCCCACTGTGATGCTTCCAGTATGAGAAATTTGGAC 329  
DB 241 TTAATAGATCAATGCTAGGAGACCCCACTGTGATGATTTTTCAGTATGAGAAATTTGGAC 300  
QY 330 CTCTTTATAGAAAAGAGCAGCGCTTTTCAGCAATTTGCTACCCATATGACATCCCTGACTAT 389  
DB 301 CTCTTTATAGAAAAGAGCAGCGCTTTTCAGCAATTTGCTACCCATATGACATCCCTGACTAT 360  
QY 390 GCATCGCTCCGGTCCATTTGATGATCTTCAGGAACTTTAGAAATTTTTCAGTATGAGAAATTTGGAC 449  
DB 361 GCATCGCTCCGGTCCATTTGATGATCTTCAGGAACTTTAGAAATTTTTCAGTATGAGAAATTTGGAC 420  
QY 450 ACATGACAGGTGTCTCACTCAAAACGGAAGAGTGGAGCTCCCAAGGGGATCAGCCGAT 509  
DB 421 ACATGACAGGTGTCTCACTCAAAACGGAAGAGTGGAGCTCCCAAGGGGATCAGCCGAT 480  
QY 510 AGTTTCTTTAGCCGACTGAATTTGGCTAAACAAATCTGAAACTCTTTACCCCACTTGAAT 569  
DB 481 AGTTTCTTTAGCCGACTGAATTTGGCTAAACAAATCTGAAACTCTTTACCCCACTTGAAT 540  
QY 570 GTGACAATGCTTAACAATAAATTTTCGACAAACTATATCATCTGGGGGATTCATCACC 629  
DB 541 GTGACAATGCTTAACAATAAATTTTCGACAAACTATATCATCTGGGGGATTCATCACC 600  
QY 630 AGCTCAAAACCAACGACGACGAGTGTGACATCCAGAAATCAGGACGAGTACAGTCTCA 689  
DB 601 AGCTCAAAACCAACGACGACGAGTGTGACATCCAGAAATCAGGACGAGTACAGTCTCA 660  
QY 690 ACACAAAGAGTCAACAAACGATAGTCCCTTAATATCGGATCTAGACCGTGGTGGG 749  
DB 661 ACACAAAGAGTCAACAAACGATAGTCCCTTAATATCGGATCTAGACCGTGGTGGG 720  
QY 750 CAATCAGGACGAGTAAGCATATATCTGAGACCACTTTGTAACCTGGAGATATCTTAATGATA 809  
DB 721 CAATCAGGACGAGTAAGCATATATCTGAGACCACTTTGTAACCTGGAGATATCTTAATGATA 780  
QY 810 AACAGTAACTCAACTAGTGTGACCGGGGATATTTTAAATTTGAAACAGGAAAGC 869  
DB 781 AACAGTAACTCAACTAGTGTGACCGGGGATATTTTAAATTTGAAACAGGAAAGC 840  
QY 870 TCTGTAATGAGATCAGATGCAACCCATAGACATTTGTGTCTGTAATTTATTCACCAAT 929  
DB 841 TCTGTAATGAGATCAGATGCAACCCATAGACATTTGTGTCTGTAATTTATTCACCAAT 900  
QY 930 GGAAGCATCCCCCAACGACAAACCACTTTCAAAATGTGAACAAAGTTACATATGAGAAATGC 989

Qy	481	GTGAGCCTCGAAAAGGGGATCGAGCCGATAGTTCTTTAGCCGACTGAATTGGCTAACAA	540
Db	505	GTGAGCCTCGAAGAAAGGGGTGAGCCGATAGTTCTTTAGCCGACTGAATTGGCTAACAA	564
Qy	541	AATCTGGAAACTCTTACCCACATGGAATGTGCAATGCCCTAACATAAAAAATTTGACA	600
Db	565	AATCTGGAATCTTACCCACATGGAATGTGCAATGCCCTAACATAAAAAATTTGATA	624
Qy	601	AATCTATACATCTGGGGATTCATCACCCGAGCTCAAAACCAACAGCAGACAGAAATTTGACA	660
Db	625	AATCTATACATCTGGGGATTCATCACCCGAGCACAACAATGAGCAGACAAAATTTGTATA	684
Qy	661	TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAAGAGTCAACAAACGATAGTCCCTTA	720
Db	685	TCCAAGAATCAGGCGAGTAACAGTCTCAACAAAAAGAGTCAACAAACAAATATCCCCA	744
Qy	721	ATATCGGATCTAGACCGTGGGTAGGGTCAATCAGGCAGGATAAGCATATATCTGGACCA	780
Db	745	ACATCGGATCTAGACCGTGGGTCAATCAGGCAGGATAAGCATATATCTGGACCA	804
Qy	781	TTGTAAACCTGGAGATATCCTAATGATAACAGTATGCGCACTTAGTTGGCACCGCGGG	840
Db	805	TTGTAAACCTGGAGATATCCTAATGATAACAGTATGCGCACTTAGTTGGCACCGCGGG	864
Qy	841	GATATTTTAAATTGAAAACAGGGAAGCTCTGTAAATGAGATCAGATGCAACCCATAGACA	900
Db	865	GATATTTTAAATGCGAAGAGGGAAGCTCTGTAAATGAGATCAGATGCAACCCATAGACA	924
Qy	901	TTTGTGTGCTGTAATGTATTACCAAAATGGAAGCATCCCCACGACAAACCACTTTCAAA	960
Db	925	CTTGTGTGCGAGTGTATTACCAAAATGGAAGCATCCCCACGACAAACCACTTTCAAA	984
Qy	961	ATGTGAACAAAGTTTACATATGGAATAATGCCCAAGTATATCAGGCACAAAACCTTTAAAGC	1020
Db	985	ATGTGAACAAAGTTACATATGGAATAATGCCCAAGTATATCAGGCACAAAACCTTTAAAGC	1044
Qy	1021	TGGCCACTGGGATGAGGAATATACGAAAAGCAAAATCAGA	1061
Db	1045	TGGCCACTGGGATGAGGAATGTACAGAAAAGCAAAATCAGA	1085

RESIST 6

RESULT 6  
A2004597

AAQ04597  
ID AAQ04597 standard: DNA: 1797 bp.XX  
ID  
AAU

AAO

XX CH XXX

DT 25-1

DT 02-0

XX

DE Equ:

XX

KW Rec

KW neu:

XX

Equation 5

XX

**FH**      **Key**

FT	CDS
1	1
2	2
3	3
4	4
5	5
6	6
7	7
8	8
9	9
10	10
11	11
12	12
13	13
14	14
15	15
16	16
17	17
18	18
19	19
20	20
21	21
22	22
23	23
24	24
25	25
26	26
27	27
28	28
29	29
30	30
31	31
32	32
33	33
34	34
35	35
36	36
37	37
38	38
39	39
40	40
41	41
42	42
43	43
44	44
45	45
46	46
47	47
48	48
49	49
50	50
51	51
52	52
53	53
54	54
55	55
56	56
57	57
58	58
59	59
60	60
61	61
62	62
63	63
64	64
65	65
66	66
67	67
68	68
69	69
70	70
71	71
72	72
73	73
74	74
75	75
76	76
77	77
78	78
79	79
80	80
81	81
82	82
83	83
84	84
85	85
86	86
87	87
88	88
89	89
90	90
91	91
92	92
93	93
94	94
95	95
96	96
97	97
98	98
99	99
100	100

ET E

13

LT  
FT

**1.3**

ET  
PT  
misa

LA  
IA  
STM

PF	21-JUL-1986;	86US-00888250.
XX		
PR	20-JUN-1985;	85US-00747020.
XX		
PA	(BIOT-) BIOTECH RES PARTNERS LTD.	
XX		
PI	Dale B, Cordell B;	
XX		
DR	WPI; 1990-163647/21.	
DR	P-PSDB; AAR04943.	
XX		
PT	Recombinant vaccines against equine influenza virus - produced using DNA	
PT	sequences encoding haemagglutinin and neuraminidase glyco-protein(s).	
XX		
PS	Disclosure; Page ?; 27pp; English.	
XX		
CC	There are nine neuraminidase (NA) subtypes and twelve haemagglutinin (HA)	
CC	subtypes. The strain carrying H3N8 glycoproteins is designated equine	
CC	influenza virus (EVI)-A2. The cDNA sequences encoding these will be	
CC	useful in the construction of diagnostic probes for the disease and of	
CC	probes for obtaining new cDNAs of the mutated form of the virus.	
CC	Recombinant vaccines are produced. See also AAQ04596-Q04599. (Updated on	
CC	25-MAR-2003 to correct PA field.)	
XX		
SQ	Sequence 1797 BP; 639 A; 341 C; 413 G; 404 T; 0 U; 0 Other;	
	Query Match 93.1%; Score 987.4; DB 2; Length 1797;	
	Best Local Similarity 95.7%; Pred. No. 1.6e-268;	
	Matches 1015; Conservative 0; Mismatches 46; Indels 0; Gaps 0;	
QY	1 AGCAAAAGCAGGGGATATTTCGTCTCAATCATGAAGACAACCAATATTTTGATACTACTGA 60	
DB	25 AGCAAAAGCAGGGGATATTTCGTCTCAATCATGAAGACAACCAATATTTTGATACTACTGA 84	
QY	61 CCCATTGGTCTACAGTCAAACCACCAACCAAGTGGAACAACACAGGCACCATTTATGTCTCG 120	
DB	85 CCCATTGGTCTACAGTCAAACCACCAACCAAGTGGAACAACACAGGCACCATTTATGTCTCG 144	
QY	121 GACACCATGCAGTAGCAAAATGGAACTTGGTAAAAACAATACTGATGACCAAAATGGAGG 180	
DB	145 GACACCATGCAGTAGCAAAATGGNACATTGGTAAAACAACTATGATGCCAAATTTGAGG 204	
QY	181 TGACAAATGCTACTGAATTAGTTTCAGAGCAATTTCAATAGGGAAAAATATGCAACAATCAT 240	
DB	205 TGACAAATGCTACTGAATTAGTTTCAGAGCACTTCAATAGGGAAAAATATGCAACAATCAT 264	
QY	241 ATAAAGTTCTAGATGCAAGAAATTCACATTAATAGATGCNATGCTAGGNACCCCACCT 300	
DB	265 ATAGGGTTCTAGATGGAAGAAATCGCACATTAATAGATGCNATGCTAGGAGATCCCCACT 324	
QY	301 GTCATGTCTTCCAGTATGAGAATTTGGGACCTCTTTCATAGAAAGACAGCGCTTTTCAGCA 360	
DB	325 GTCATGTCTTTCAGTATGAGAATTTGGGACCTCTTTCATAGAAAGACAGCGCTTTTCAGCA 384	
QY	361 ATTGCTACCCATATGATACCTCCCTGACTATGCAATCGCTCCGGTCCATTTGTAGCATCCTCAG 420	
DB	385 ATTGCTACCCATATGATACCTCCCTGACTATGCAATCGCTCCGGTCTATTGTGGCATCTTCAG 444	
QY	421 GAACATTAGAAATTCACAGCAGAGGGATTACATGGAACAGGTGTCACTCAAAACGGGAAGAA 480	
DB	445 GAACATTAGAAATTCACAGCAGAGGGATTACATGGAACAGGTGTCACTCAAAACGGGAAGAA 504	
QY	481 GTSGAGCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTTGCTTAACAA 540	
DB	505 GTSGAGCCTGCAAGAGGGGTGAGCCGATAGTTTCTTTAGCCGACTGAATTTGCTTAACAA 564	
QY	541 AATCTCTGAAACTCTTACCCTCAATTTGAATGTGCAATGCTCTAACATAAAAAATTTTCGACA 600	
DB	565 AATCTGMAAATCTTACCCTCAATTTGAATGTGCAATGCTCTAACATAAAAAATTTTCGATA 624	
QY	601 AACTATACATCTGGGGATTCATCACCCGAGCTCAAAACAAACAGCAGACAGAAATTTGTACA 660	
DB	625 AACTATACATCTGGGGATTCATCACCCGAGCACAACCAATGAGCAGACAAAATTTGTATA 684	

QY 241 AFAAGTCTTAGATGAAGAATAATGACATTAATAGATGCAATGCTAGAGACCCCACT 300  
DB 241 ATAGGGTTCTAGATGAAGAATAATGACATTAATAGATGCAATGCTAGAGACCCCACT 300  
QY 301 GTGATGCTCTCCAGTATGAGAAATGGGACCTCTTCATAGAAAGAAGCAGCGCTTTTCAGCA 360  
DB 301 GTGATGCTCTCCAGTATGAGAAATGGGACCTCTTCATAGAAAGAAGCAGCGCTTTTCAGCA 360  
QY 361 ATTGCTACCCATATGACATCCCTGACTATGCAATGCTCGGTCCTATGAGCATCCTCAG 420  
DB 361 ATTGCTACCCATATGACATCCCTGACTATGCAATGCTCGGTCCTATGAGCATCCTCAG 420  
QY 421 GAACATTAGAAATTCACAGAGAGGGATTCACATGACAGGCTGCTCACTCAAAACGGAAGA 480  
DB 421 GAACATTAGAAATTCACAGAGAGGGATTCACATGACAGGCTGCTCACTCAAAACGGAAGA 480  
QY 481 GTGGAGCCTGCAAAAGGGATCAGCGGATAGTCTTTAGCCGACTGAATGGCTAAACAA 540  
DB 481 GTGGAGCCTGCAAAAGGGATCAGCGGATAGTCTTTAGCCGACTGAATGGCTAAACAA 540  
QY 541 AATCTGGAACCTCTTACCCCAATGGAATGTGCAATGCTCACTCAATAAATTTTCGACA 600  
DB 541 AATCTGGAACCTCTTACCCCAATGGAATGTGCAATGCTCACTCAATAAATTTTCGACA 600  
QY 601 AACTATACATCTGGGGATTCATCACCAGCTCAACCAACAGCAGACAGAAATTTGTACA 660  
DB 601 AACTATACATCTGGGGATTCATCACCAGCTCAACCAACAGCAGACAGAAATTTGTACA 660  
QY 661 TCCAGAAATCAGGACGAGTAACAGTCTCAACAAAAAGAAAGTCAACAAACGATAGTCCCTA 720  
DB 661 TCCAGAAATCAGGACGAGTAACAGTCTCAACAAAAAGAAAGTCAACAAACGATAGTCCCTA 720  
QY 721 ATATCGATCTAGACCGTGGGTTAGGGTCAATCAGGCAAGGATAGCATATATCTGACCA 780  
DB 721 ATATCGATCTAGACCGTGGGTTAGGGTCAATCAGGCAAGGATAGCATATATCTGACCA 780  
QY 781 TTGTAAACCTGAGATATCTTAATGATAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 840  
DB 781 TTGTAAACCTGAGATATCTTAATGATAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 840  
QY 841 GATATTTTAAATGAAAAAGGAAAGCTCTGTAATGATGATGATGATGATGATGATGATGAT 900  
DB 841 GATATTTTAAATGAAAAAGGAAAGCTCTGTAATGATGATGATGATGATGATGATGATGAT 900  
QY 901 TTTGTGTCTGAATGATTAACCAATGGAGGATCCCAACGACAAACCAATTTTCAAA 960  
DB 901 CTTGTGTCTGAATGATTAACCAATGGAGGATCCCAACGACAAACCAATTTTCAAA 960  
QY 961 ATGTGAACAAAGTTACATATGGAATGCCCCAAGTATATCAGGCAAAACACTTTTAAAGC 1020  
DB 961 ATGTGAACAAAGTTACATATGGAATGCCCCAAGTATATCAGGCAAAACACTTTTAAAGC 1020  
QY 1021 TGGCCACTGGGATCAGGAATATACAGAAAGCAAAATTCAGA 1061  
DB 1021 TGGCCACTGGGATCAGGAATATACAGAAAGCAAAATTCAGA 1061

RESULT 5

AAN71067  
ID AAN71067 standard; DNA; 1788 BP.

XX AAN71067;

AC 08-MAR-1991 (first entry)

XX Sequence encoding equine influenza virus strain H3N8 (EIV-A2)  
DE haemagglutinin protein H3.

XX HA; vaccine; Vaccina; ds.

XX Equine influenza virus.

XX Key Location/Qualifiers

CDS  
FT mat\_peptide 54..1748  
FT mat\_peptide /\*tag= a  
FT mat\_peptide 102..1082  
FT mat\_peptide /\*tag= b  
FT mat\_peptide /label= HA 1  
FT mat\_peptide 1086..1748  
FT mat\_peptide /\*tag= c  
FT mat\_peptide /label= HA 2  
XX WO8607593-A.  
PN 31-DEC-1986.  
XX 20-JUN-1986; 86WO-US001343.  
XX 20-JUN-1985; 85US-00747020.  
XX (BIOT-) BIOTECHN RES PARTNE.  
XX Dale B, Cordell B;  
XX WPI; 1987-007191/01.  
XX P-PSDB; AAP70711.  
XX Preventing equine influenza virus infection - using recombinant vaccines produced using DNA sequences encoding haemagglutinin and neuraminidase glyco:proteins.  
XX Disclosure; Fig 2; 63pp; English.  
XX Peptides derived from the haemagglutinin H7 and H3 and neuraminidase N7 and N8 genes may be used to derive antigenic peptides useful in vaccination against equine influenza virus infection. Abs raised to the peptides may be used in diagnosis of the infection and construction of probes to mutated forms of the virus  
SQ Sequence 1788 BP; 637 A; 340 C; 409 G; 402 T; 0 U; 0 Other;

Query Match 93.1%; Score 987.4; DB 1; Length 1788;  
Best Local Similarity 95.7%; Pred. No. 1.6e-268;  
Matches 1015; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 AGCAAAAGCAGGGGATATTTCTGCAATCATGAGAACCAACCATTTATTTGATACTACTGA 60  
DB 25 AGCAAAAGCAGGGGATATTTCTGCAATCATGAGAACCAACCATTTATTTGATACTACTGA 84  
QY 61 CCCATTGGTCTACAGTCAAAACCCCAACCCAGTGGAAACACACACACCATTTATCTGG 120  
DB 85 CCCATTGGTCTACAGTCAAAACCCCAACCCAGTGGAAACACACACACCATTTATCTGG 144  
QY 121 GACACATGCTAGTCAAAATGGAACATTTGGTAAACCAATTAATGATGACCAAAATTTAGG 180  
DB 145 GACACATGCTAGTCAAAATGGAACATTTGGTAAACCAATTAATGATGACCAAAATTTAGG 204  
QY 181 TGACAAATGCTACTGAAATTTAGTTCAGAGCATTTCAATAGGGAATATGCAACCACTCAT 240  
DB 205 TGACAAATGCTACTGAAATTTAGTTCAGAGCATTTCAATAGGGAATATGCAACCACTCAT 264  
QY 241 ATAAAGTTCTAGATGGAAGAAATTCACATTAATAGATGCAATGCTAGGAGACCCCACT 300  
DB 265 ATAGGGTTCTAGATGGAAGAAATTCACATTAATAGATGCAATGCTAGGAGATCCCACT 324  
QY 301 GTGATGCTCTCCAGTATGAGAAATGGGACCTCTTCATAGAAAGAAGCAGCGCTTTTCAGCA 360  
DB 325 GTGATGCTCTCCAGTATGAGAAATGGGACCTCTTCATAGAAAGAAGCAGCGCTTTTCAGCA 384  
QY 361 ATTGCTACCCATATGACATCCCTGACTATGCAATGCTCGGTCCTATGAGCATCCTCAG 420  
DB 385 ATTGCTACCCATATGACATCCCTGACTATGCAATGCTCGGTCCTATGAGCATCCTCAG 444  
QY 421 GAACATTAGAAATTCACAGCAGAGGGATTCACATGACAGGCTGCTCACTCAAAACGGAAGA 480  
DB 445 GAACATTAGAAATTCACAGCAGAGGGATTCACATGACAGGCTGCTCACTCAAAACGGAAGA 504

Db	61	AGTGGCAACAAACACAGCCACATTAATGCTCTGGGACCACTCATGAGTAGCAAAATGGAAACATTTG	120
Qy	150	GTAAAAACAATAACTGATGACCAAAATGGAGTGACAAATGCTACTGAAATAGTTTCAGAGC	209
Db	121	GTAAAAACAATAACTGATGACCAAAATGGAGTGACAAATGCTACTGAAATAGTTTCAGAGC	180
Qy	210	ATTTCAATAGGGAAATATGCAACAACTCATATAAAGTTCTTAGNTGGAAGAAATTGACACA	269
Db	181	ATTTCAATAGGGAAATATGCAACAACTCATATAGAGTTCTTAGATGGAAGAAATTGACACA	240
Qy	270	TTAATAGATGCAATGCTAGGAGACCCCACTGTGTGATGCTTTCCAAGTATGAGAAATTTGGGAC	329
Db	241	TTAATAGATGCAATGCTAGGAGACCCCACTGTGTGATGCTTTCAATGATGAGAAATTTGGGAC	300
Qy	330	CTCTTCATGAAGAAGACGAGCGCTTTTCAGCAATTTGCTACCCATATGACATCCCTGACTAT	389
Db	301	CTCTTCATGAAGAAGACGAGCGCTTTTCAGCAATTTGCTACCCATATGACATCCCTGACTAT	360
Qy	390	GCATCGCTCCGGTCCATTTGTAGCATCTCTCAGGACATTAGAATTCACAGCAGAGGATTC	449
Db	361	GCATCGCTCCGGTCCATTTGTAGCATCTCTCAGGACATTTGGAATTCACAGCAGAGGATTC	420
Qy	450	ACATGGACAGGTGTCACTCAAAAACGGAAGATGGAGCCTGCAAAAAGGGCATCAGCCGAT	509
Db	421	ACATGGACAGGTGTCACTCAAAAACGGAAGATGGAGCCTGCAAAAAGGGCATCAGCCGAT	480
Qy	510	AGTTCTTTTAGCCGACTGAATTTGGCTAAACAAATCTGGAACCTCTTACCCCAATTTGAAT	569
Db	481	AGTTCTTTTAGCCGACTGAATTTGGCTAAACAAATCTGGAACCTCTTACCCCAATTTGAAT	540
Qy	570	GTGACATGCTTAACATAAATAATTTTCGACAAACTATACATCTGGGGGATTCATCACC	629
Db	541	GTGACATGCTTAACATAAATAATTTTCGACAAACTATACATCTGGGGGATTCATCACC	600
Qy	630	AGCTCAAAACCAACAGCAGACAGAAATTTGATCAATCCAAGAAATCAGGACAGGTAAACAGTCTCA	689
Db	601	AGCTCAAAACCAACAGCAGACAGAAATTTGATCAATCCAAGAAATCAGGACAGGTAAACAGTCTCA	660
Qy	690	ACAAAAAGAGTCAACAAACGATAGTCCCTTAATTCGGATCTAGACCGTGGGTTAGGGGT	749
Db	661	ACAAAAAGAGTCAACAAACGATAGTCCCTTAATTCGGATCTAGACCGTGGGTTAGGGGT	720
Qy	750	CAATCAGCAGGATTAAGCATATATCTGCACCAATTTGTAACCTGGAGATATCCCTAATGATA	809
Db	721	CAATCAGCAGGATTAAGCATATATCTGCACCAATTTGTAACCTGGAGATATCCCTAATGATA	780
Qy	810	AACAGTAAATGGCAACTTAGTTTGCAACCGCGGGATTAATTTAAATTTGAAAAACAGGAAAAAGC	869
Db	781	AACAGTAAATGGCAACTTAGTTTGCAACCGCGGGATTAATTTAAATTTGAAAAACAGGAAAAAGC	840
Qy	870	TCTGTAAATGAGATCAGATGCACCCATAGACATTTGTGTGTCTGAATGTATTTACACCAAT	929
Db	841	TCTGTAAATGAGATCAGATGCACCCATAGACATTTGTGTGTCTGAATGTATTTACACCAAT	900
Qy	930	GGAGAGCATCCCAACGACAAACCATTTTCAAAATGTGAACAAAGTTACATATGGAAAAATGC	989
Db	901	GGAGAGCATCCCAACGACAAACCATTTTCAAAATGTGAACAAAGTTACATATGGAAAAATGC	960
Qy	990	CCCAAGTATATCAGGCAAAAACATTTTAAAGCTGGCCACTCGGATGAGGAATATACACGAA	1049
Db	961	CCCAAGTATATCAGGCAAAAACATTTTAAAGCTGGCCACTCGGATGAGGAATATACACGAA	1020
Qy	1050	AAGCAAAATCAGA	1061
Db	1021	AAGCAAAATCAGA	1032

DT	25-MAR-2003 (revised)	
DT	24-FEB-1993 (first entry)	
XX		
DE	EIV HA (A2/Suffolk/89).	
XX		
KW	Equine influenza virus; EIV; hemagglutinin; HA; A2/Suffolk/89;	
KW	expression cassette; NYVAC; ALVAC; recombinant vector; M13;	
KW	polymerase chain reaction; PCR; vaccinia virus; I3L promoter;	
KW	canarypox virus; Copenhagen vaccine strain; virulence factor;	
KW	deletion loci; recipient loci; ss.	
XX		
OS	Synthetic.	
XX		
PN	WO9215672-A1.	
XX		
PD	17-SEP-1992.	
XX		
PF	09-MAR-1992; 92WO-US001906.	
XX		
PR	07-MAR-1991; 91US-00666056.	
PR	11-JUN-1991; 91US-00713967.	
PR	06-MAR-1992; 92US-00847951.	
XX		
PA	(VIRO-) VIROGENETICS CORP.	
XX		
PI	Paoletti E, Perkus ME, Taylor J, Tartaglia J, Norton EK;	
PI	Riviere M, De Taïne C, Limbach KJ, Johnson GP, Pincus SE, Cox WI;	
XX	Francis J, Gettig RR;	
XX		
DR	WPI; 1992-331718/40.	
XX		
PT	Vaccine comprises recombinant, attenuated pox-virus - use for vaccinating	
PT	against viral infections such as rabies, hepatitis B, HIV, HSV, EBV, CMV,	
PT	mumps etc.	
XX		
PS	Disclosure; Fig 25; 456pp; English.	
XX		
CC	The sequence given encodes the equine influenza virus (EIV) hemagglutinin	
CC	(HA) (A2/Suffolk/89). This sequence was used to generate an expression	
CC	cassette for the insertion of the EIV HA gene into NYVAC and ALVAC	
CC	recombinant vectors. The HA gene sequence was isolated by polymerase	
CC	chain reaction from an M13 clone. Some non-conserved base-changes were	
CC	observed due to the amplification process. The EIV HA gene was linked to	
CC	the I3L promoter and inserted into a vaccinia insertion plasmid deleted	
CC	for ORP's C6L-K1L. NYVAC is derived from a Copenhagen vaccine strain of	
CC	vaccinia virus and ALVAC is derived from a canarypox virus which has been	
CC	modified by deletion of non-essential regions of the genome encoding	
CC	known or potential virulence factors. The deletion loci of both vectors	
CC	were engineered as recipient loci for the insertion of foreign genes. See	
CC	also AAQ35501-864. (Updated on 25-MAR-2003 to correct PN field.)	
XX		
SQ	Sequence 1762 BP; 637 A; 328 C; 384 G; 412 T; 0 U; 1 Other;	

RESULT 4  
AAQ29112  
ID AAQ29112 standard; DNA; 1762 BP.  
XX  
XX  
YY

CC or treating infections caused by influenza A viruses in animals,  
CC particularly horses. The present sequence is a DNA (neihw1762) encoding  
CC wild type equine influenza virus H3N8 haemagglutinin (HA) protein denoted  
CC as PeiWHA565. This sequence is modified to generate cold-adapted equine  
CC influenza virus  
XX  
SQ Sequence 1762 BP; 639 A; 334 C; 383 G; 406 T; 0 U; 0 Other;

Query Match 97.3%; Score 1032.2; DB 3; Length 1762;  
Best Local Similarity 98.3%; Pred. No. 3.5e-281;  
Matches 1043; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 AGCAAAAGCAGGGATATTTCTGTCATCATGAAGACAACCACTATTTTGATACTACTGA 60  
DB 1 AGCAAAAGCAGGGATATTTCTGTCATCATGAAGACAACCACTATTTTGATACTACTGA 60  
QY 61 CCATTGGGTCTACAGTCAAAACCCCAACCAAGTGGAAACCAACACAGCCACATTATGCTGG 120  
DB 61 CCATTGGGTCTACAGTCAAAACCCCAACCAAGTGGAAACCAACACAGCCACATTATGCTGG 120  
QY 121 GACACATGAGTAGCAAAATGGAACATTTGGTAAACCAATTAAGTGAACCAATTTGAGG 180  
DB 121 GACACATGAGTAGCAAAATGGAACATTTGGTAAACCAATTAAGTGAACCAATTTGAGG 180  
QY 181 TGACAAATGCTACTGAAATAGTTCAGAGCATTTCAATAGGGAATAATGCAACAACTCAT 240  
DB 181 TGACAAATGCTACTGAAATAGTTCAGAGCATTTCAATAGGGAATAATGCAACAACTCAT 240  
QY 241 ATAAAGTTCTAGATGGAAGAAATTCACATTAATAGATGCAATGCTAGGAGACCCCACT 300  
DB 241 ATAGAGTTCTAGATGGAAGAAATTCACATTAATAGATGCAATGCTAGGAGACCCCACT 300  
QY 301 GTGATGCTTCCAGTATGAGAAATGGGACCTCTTCATAGAAAGAGCAGCGCTTTCAGCA 360  
DB 301 GTGATGCTTCCAGTATGAGAAATGGGACCTCTTCATAGAAAGAGCAGCGCTTTCAGCA 360  
QY 361 ATGTCTACCCATATGATCCCTGACTATGTCATCGCTCCGCTCCATTTAGCATCTCTAG 420  
DB 361 GTTGCTACCCATATGATCCCTGACTATGTCATCGCTCCGCTCCATTTAGCATCTCTAG 420  
QY 421 GAACATTAGAAATTCACAGAGAGGAAATTCATATGGAAGAGTGTCTCAATAACCGAGAA 480  
DB 421 GAACATTAGAAATTCACAGAGAGGAAATTCATATGGAAGAGTGTCTCAATAACCGAGAA 480  
QY 481 GTGAGCGCTGCAAAAGGGATCAGCGATAGTTCTTTAGCGAGTGAATTTGCTTAACAA 540  
DB 481 GTGAGCGCTGCAAAAGGGATCAGCGATAGTTCTTTAGCGAGTGAATTTGCTTAACAA 540  
QY 541 AATCTGGAATCTTACCCACATTTGAATGTGCAATGCTTAACATAAAAAATTTGACA 600  
DB 541 AATCTGGAATCTTACCCACATTTGAATGTGCAATGCTTAACATAAAAAATTTGACA 600  
QY 601 AACTATACATCTGGGGATTCATCACCGAGTCAAAACCAAGCAGAGAGAAATTTGACA 660  
DB 601 AACTATACATCTGGGGATTCATCACCGAGTCAAAACCAAGCAGAGAGAAATTTGACA 660  
QY 661 TCCAGAAATCAGACGAGTAACAGTCTCAACAAAAAGAGTCAACAAACGATAGTCCCTTA 720  
DB 661 TCCAGAAATCAGACGAGTAACAGTCTCAACAAAAAGAGTCAACAAACGATAGTCCCTTA 720  
QY 721 ATATCGGATCTAGACCGTGGGTTAGGGGTCAATCAGGCGAGGATAAGCATATATGAGCA 780  
DB 721 ATATCGGATCTAGACCGTGGGTTAGGGGTCAATCAGGCGAGGATAAGCATATATGAGCA 780  
QY 781 TTGTAAACCTGAGATATCTTAATGATAACAGTAAATGGCACTTATGTCACCGCGGG 840  
DB 781 TTGTAAACCTGAGATATCTTAATGATAACAGTAAATGGCACTTATGTCACCGCGGG 840  
QY 841 GATATTTAAATTTGAAAACAGGAAAGCTCTGTAATGAGATCAGATGCAACCCATAGACA 900  
DB 841 GATATTTAAATTTGAAAACAGGAAAGCTCTGTAATGAGATCAGATGCAACCCATAGACA 900  
QY 901 TTTGTGTCTGAATGATTTATACCAAAATGGAAGCATTCGCCAACGACAAACCAATTTCAA 960

DB 901 TTTGTGTCTGAATGATTTACCAAAATGGAAGCATCCCAACGACAAACCAATTTCAA 960  
QY 961 ATGTGAACAAGTTTACATATGGAATGCCCAAGTATATCAGGCAAAACCACTTTAAGC 1020  
DB 961 ATGTGAACAAGTTTACATATGGAATGCCCAAGTATATCAGGCAAAACCACTTTAAGC 1020  
QY 1021 TGGCCACTGGGATGAGGAATATACCAAAAAGCAAAATCAGA 1061  
DB 1021 TGGCCACTGGGATGAGGAATATACCAAAAAGCAAAATCAGA 1061  
RESULT 3  
AAZ30213  
ID AAZ30213 standard; DNA; 1698 BP.  
XX  
AC AAZ30213;  
DT 11-FEB-2000 (first entry)  
XX  
Sequence of the haemagglutinin (HA) gene of EIV strain Kentucky 1/94.  
DE Haemagglutinin gene; EIV; strain Kentucky 1/94; DNA vaccine; horse;  
KW acrylic acid polymer; methacrylic acid polymer; copolymer;  
KW maleic anhydride; alkenyl derivative; animal vaccine; viral infection;  
KW bacterial infection; ss.  
XX  
OS Equine influenza virus.  
XX  
FR2776928-A1.  
XX  
08-OCT-1999.  
XX  
03-APR-1998; 98FR-00004409.  
XX  
03-APR-1998; 98FR-00004409.  
XX  
(MERI-) MERIAL SAS.  
XX  
Audonnet JCF, Minke JM;  
XX  
WPI; 1999-593389/51.  
XX  
Vaccine containing naked DNA and acrylic acid polymer or maleic anhydride  
copolymer, for protection against viral or bacterial diseases in animals.  
XX  
Example 9; Fig 2; 34pp; French.  
XX  
The present sequence represents the haemagglutinin gene of Equine  
influenza virus (EIV) strain Kentucky 1/94. The sequence was used to  
prepare a DNA vaccine for horses, representative of the DNA vaccines of  
the invention. The specification describes a DNA vaccine that comprises  
naked DNA encoding an antigenic polypeptide, and at least one adjuvant  
that is an acrylic or methacrylic acid polymer or a copolymer of maleic  
anhydride with an alkenyl derivative. The vaccines are simple and easy to  
prepare (simply by mixing components) and they do not involve any strong  
interactions between DNA and other components that are likely to cause  
complex formation. The vaccines are used to protect animals (pigs,  
horses, dogs, cattle, cats or birds) against a wide variety of viral or  
bacterial infections.  
SQ Sequence 1698 BP; 618 A; 320 C; 369 G; 391 T; 0 U; 0 Other;  
Query Match 96.1%; Score 1019.2; DB 2; Length 1698;  
Best Local Similarity 99.2%; Pred. No. 1.6e-277;  
Matches 1024; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
QY 30 ATGAGACAACCACTATTTTGATATCTACTGCCCATTTGGTCTACATCAAAACCAAC 89  
DB 1 ATGAGACAACCACTATTTTGATATCTACTGCCCATTTGGTCTACATCAAAACCAAC 60  
QY 90 AGTGGAAACACACAGCCACCACTTATGCTGGGACACCATGAGTACCAATGCAATG 149



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 01:41:16 ; Search time 672 Seconds  
(without alignments)  
9346.496 Million cell updates/sec

Title: US-10-826-929A-1  
Perfect score: 1061  
Sequence: 1 agcaaaagcagggatattt.....taccagaaaagcaaatcaga 1061

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 4390206 seqs, 2959870667 residues  
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : N\_Geneseq\_16Dec04:\*
- 1: Geneseqn1980s:\*
  - 2: Geneseqn1990s:\*
  - 3: Geneseqn2000s:\*
  - 4: Geneseqn2001as:\*
  - 5: Geneseqn2001bs:\*
  - 6: Geneseqn2002as:\*
  - 7: Geneseqn2002bs:\*
  - 8: Geneseqn2003as:\*
  - 9: Geneseqn2003bs:\*
  - 10: Geneseqn2003cs:\*
  - 11: Geneseqn2003ds:\*
  - 12: Geneseqn2004as:\*
  - 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1033.8	97.4	1762	3	Aaz50976 Cold-adap
2	1032.2	97.3	1762	3	Aaz50975 Wild type
3	1019.2	96.1	1698	2	Aaz30213 Sequence
4	1018.4	96.0	1762	2	Aaz29112 EIV HA (A
5	987.4	93.1	1788	1	Aan71067 Sequence
6	987.4	93.1	1797	2	Aaq04597 Equine he
7	984	92.7	1698	2	Aaz30211 Sequence
8	984	92.7	1698	3	Aaz47007 Equine in
9	976.2	92.0	1762	2	Aaz29111 EIV HA (A
10	947.2	89.3	1698	2	Aav49391 EIV Fonta
11	607.2	57.2	1777	2	Aaq072855 Full leng
12	601.6	56.7	1765	6	ABA93937 Influenza
13	598.4	56.4	1764	6	ABA93944 Influenza
14	585.6	55.2	1762	1	Aan70642 Sequence
15	566.2	53.4	1091	6	ABq82724 Influenza
16	558.2	52.6	1653	6	ABq82723 Influenza
17	556	52.4	987	6	ABq82726 Influenza
18	554.4	52.3	987	6	ABq82725 Influenza
19	549.2	51.8	1793	2	Aat59212 Influenza
20	549.2	51.8	1793	2	Aax00773 Influenza

21	549.2	51.8	1793	5	AAD09586 Influenza
22	546.4	51.5	988	12	ADO15237 Influenza
23	544.4	51.3	1757	2	AAT59216 Influenza
24	544.4	51.3	1757	2	AAX00777 Influenza
25	544.4	51.3	1757	5	AAD09590 Influenza
26	541.2	51.0	1701	2	AAV49298 SIV stral
27	541.2	51.0	1757	2	AAT59219 Influenza
28	541.2	51.0	1757	2	AAX00780 Influenza
29	541.2	51.0	1757	5	AAD09593 Influenza
30	150.4	14.2	1809	1	AAN71066 Sequence
31	150.4	14.2	1809	2	AAQ04596 Equine he
32	148.2	14.0	1759	2	AAQ29110 EIV HA (A
33	133.4	12.6	2005	3	AAA75002 Nucleotid
34	133.4	12.6	4610	3	AAA75005 Nucleotid
35	133.4	12.6	4930	3	AAA75000 Nucleotid
36	127.2	12.0	1721	2	ADH29821 Swinepox
37	127.2	12.0	1721	2	AAV26247 Genomic D
38	125.2	11.8	1711	6	AAI50113 Recombina
39	123.8	11.7	1742	1	AAN00004 Sequence
40	123.6	11.6	1733	10	ADF28972 Influenza
41	122.6	11.6	1775	12	ADO15246 Influenza
42	122.4	11.5	1110	2	AAQ72807 DNA encod
43	121.4	11.4	1724	3	AAA76188 Swine inf
44	117.4	11.1	1701	2	AAV49294 SIV stral
45	116.2	11.0	1692	12	ADO15232 Influenza

ALIGNMENTS

RESULT 1  
AAZ50976  
ID AAZ50976 standard; DNA; 1762 BP.  
XX  
AC AAZ50976;  
XX  
DT 05-JUN-2000 (first entry)  
XX  
DE Cold-adapted equine influenza virus H3N8 haemagglutinin protein DNA.  
XX  
KW Haemagglutinin protein; modified HA protein; horse; cold-adaptation;  
KW reassortant virus; temperature sensitivity; dominant interference;  
KW attenuation; antiviral; vaccine; prevention; treatment;  
KW influenza A virus infection; ds.  
XX  
OS Equine influenza virus H3N8.  
XX  
FH Key Location/Qualifiers  
CDS 30..1727  
FT /\*tag= a  
FT /product= "HA protein"  
FT /note= "The coding region without the stop codon is  
FT specifically claimed"

XX WO200009702-A1.  
XX 24-FEB-2000.  
XX  
XX 12-AUG-1999; 99WO-US018583.  
XX  
XX 13-AUG-1998; 98US-00133921.  
XX (UYPI-) UNIV PITTSBURGH.  
XX Dowling PW, Youngner JS;  
XX WPI; 2000-224339/19.  
XX P-PSDB; AAY70057.  
XX  
XX New cold-adapted equine influenza viruses and reassortant viruses used as  
XX vaccines for treating influenza infections in animals, particularly  
XX horses, have a phenotype such as temperature sensitivity or dominant  
XX interference.

DB: 14 Gaps: 0  
 US-10-826-929A-1 (1-1061) x US-10-105-232-284 (1-39)  
 QY 858 ACAGGAAAAGCTCTGTAAATGAGATCAGATGCACCCATAGACATTTGTGTCTGAATGT 917  
 Db 2 ThrGlySerSerValMetArgSerAspAlaProIleAspPheCysAsnSerGluCys 21  
 QY 918 ATTACACCAAAATGGAAGCATCCCAACGACAAACCATTTCAAATGTGAACAAA 971  
 Db 22 IleThrProAsnGlnSerIleProAsnAspLysProPheGlnAsnValAsnLys 39

Search completed: February 27, 2005, 18:56:49  
 Job time : 166.5 secs



; PRIOR APPLICATION NUMBER: 60/278,761  
 ; PRIOR FILING DATE: 2001-03-27  
 ; NUMBER OF SEQ ID NOS: 729  
 ; SOFTWARE: PatentIn 2.1  
 ; SEQ ID NO 270  
 ; LENGTH: 47  
 ; TYPE: PRT  
 ; ORGANISM: Influenza virus  
 US-10-189-437-270

Alignment Scores:  
 Pred. No.: 1.3e-13 Length: 47  
 Score: 225.00 Matches: 41  
 Percent Similarity: 91.30% Conservativeness: 1  
 Best Local Similarity: 89.13% Mismatches: 4  
 Query Match: 11.77% Indels: 0  
 DB: 14 Gaps: 0

US-10-826-929A-1 (1-1061) x US-10-189-437-270 (1-47)

QY 858 ACAGGGAAGGCTCTGTATGAGATCAGATGACCCATAGACATTTGTGTCTGAATGT 917  
 Db 2 ThrGlyLysSerSerValMetArgSerAspAlaProIleAspPheCysAsnSerGluCys 21  
 QY 918 ATTACCAAAATGGAAGCATCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACA 977  
 Db 22 IleThrProAsnGlnSerIleProAsnAspLysProPheGlnAsnValAsnLysIleThr 41  
 QY 978 TATGGAATGCCCAAG 995  
 Db 42 TyrGlyAlaCysProLys 47

#### RESULT 13

US-10-381-530-30;  
 ; Sequence 30, Application US/10381530  
 ; Publication No. US20040137013A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KATINGER, Hermann  
 ; APPLICANT: EGOROV, Andre  
 ; APPLICANT: FERKO, Boris  
 ; APPLICANT: ROMANOVA, Julia  
 ; APPLICANT: KATINGER, Diemar  
 ; TITLE OF INVENTION: LIVE VACCINE AND METHOD OF MANUFACTURE  
 ; FILE REFERENCE: P/167-134  
 ; CURRENT APPLICATION NUMBER: US/10/381,530  
 ; CURRENT FILING DATE: 2003-11-24  
 ; PRIOR APPLICATION NUMBER: PCT/EP01/11087  
 ; PRIOR FILING DATE: 2001-09-25  
 ; PRIOR APPLICATION NUMBER: 00120896.6  
 ; PRIOR FILING DATE: 2000-09-25  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 30  
 ; LENGTH: 584  
 ; TYPE: PRT  
 ; ORGANISM: Influenza B/Vienna/1/99/ca  
 US-10-381-530-30

Alignment Scores:  
 Pred. No.: 4.97e-13 Length: 584  
 Score: 222.00 Matches: 88  
 Percent Similarity: 39.11% Conservativeness: 61  
 Best Local Similarity: 23.10% Mismatches: 170  
 Query Match: 11.61% Indels: 62  
 DB: 16 Gaps: 16

US-10-826-929A-1 (1-1061) x US-10-381-530-30 (1-584)

QY 30 ATGAAGACAAACCATTTTGTATCTACTGACCCCATTTGGTCTACAGTCAAAACCCCAACC 89  
 Db 1 MetLysAlaIleValLeuLeuMetValVal-----  
 QY 90 AGTGGAAACAAACAGCCACCATTTATGTCTGGGACCACTGACAGTCAAAATGGAACATTG 149

Db 12 ---ThrSerAsnAlaAspArgIleCysThrGlyIleThrSerSerAsnSerProHisVal 30  
 QY 150 GTAAACAAATAACTGATGACCAAAATTCAGGTGCAAAATGCTACTGAATAGTTAGTTAG--- 206  
 Db 31 ValLysThrAlaThrGlnGlyValAsnValThrGlyAlaIleProLeuThrThrThr 50  
 QY 207 -----AGCATTTCAATAGGGAATAATATGCAAC 233  
 Db 51 ProThrLysSerHisPheAlaAsnLeuLysGlyThrLysThrArgGlyLysLeuCysPro 70  
 QY 234 AACTCATATAAGTTCTAGATGGAAGAAATTCACATTAATAGATGCAATGCTAGACAGAC 293  
 Db 71 ThrCysLeu-----AsnCysThrAspLeuAspValAlaLeuGlyArg 84  
 QY 294 CCCCACTGT---GATGCTCTCCAGTATGAGAATTTGGGACCTCTTCATAGAAAGACGACG 350  
 Db 85 ProMetCysValGlyIleThrProSerAlaLysAlaSerIleLeuHisGluValArgPro 104  
 QY 351 GCTTTGACCAATTCCTACCCA-----TATGACATCCCTGACTATGTCATCGCTCCGGTCC 404  
 Db 105 ValThrSerGlyCysPheProIleMetHisaspArgThrLysIleArgGlnLeuProAsn 124  
 QY 405 ATTGTAGCATCCTCAGGAACATTAAGATTCACAGCAGAGGAGATTCCATGAGACA----- 458  
 Db 125 LeuLeuArgGlyTyrGluLysIleArgLeuSerThrGlnAsnValIleAsnThrGluLys 144  
 QY 459 -----GGTGTCACCTCAAAACGGAAGAGATTTGGGCTCCCAAAAGGGGATCAGCCGAT 509  
 Db 145 AlaProGlyGlyProTyrArgLeuGlyThrSerGlySerCysProAsnAlaThrSerLys 164  
 QY 510 AGT---TCTTTAGCCGACTGAATTTGGCTAAACAAATCTGGAACCTCTTACCCACATTG 566  
 Db 165 SerGlyPhePheAlaThrMetAlaTrpAlaValProArgAspAsnAsnLysThrAlaThr 184  
 QY 567 AAT-----GTGACAATGCCTAAC-----AATAAAATTTGCAACAACTATACATC 611  
 Db 185 AsnProLeuThrValGluValProHisIleCysThrLysGluGluAspGlnIleThrVal 204  
 QY 612 TGGGGGATTTCATCCCGGCTCAACCAACAGCAGACAGAGATTGTATACCAAGATCA 671  
 Db 205 TrpGlyPheHisSerAspAsnLysThrGlnMetLysAsnLeuTyrGlyAspSerAsnPro 224  
 QY 672 GGACGAGTAACAGCTCTCAACAAAGAGAGTCAACAAACGATAGTCCCTAAATATCCGATCT 731  
 Db 225 GlnLysPheThrSerSerAlaAsnGlyIleThrThrHisTyrValSerGlnIleGlyGly 244  
 QY 732 AGACCG-----TGGGTTAGGGGTCAATCAGGAGGATTAAGCATATAGTGG 776  
 Db 245 PheProAspGlnThrGluAspGlyGlyLeuProGlnSerGlyArgIleValValAspTyr 264  
 QY 777 ACCATTGTAAACCTGGAGATATCCTAATGATAACAGTAAATGGCAACTTAGTTGCACCG 836  
 Db 265 MetValGlnLysProGly-----LysThrGlyThrIleValTyrGln 278  
 QY 837 CGGGGATATTTTAAA-----TTGAAACACAGGGAAGCTCTGTATATGAGA 881  
 Db 279 ArgGlyIleLeuLeuProGlnLysValTrpCysAlaSerGlyArgSerLysValIleLys 298  
 QY 882 TCAGATGACCCATGACATTTGTGTCTGAATGTATTATACACCAAT---GGAAGCATC 938  
 Db 299 GlySerLeuProLeu---IleGlyGluAlaAspCysLeuHisGluLysTyrGlyGlyLeu 317  
 QY 939 CCCAACGACAAACCA---TTTCAAAATGTGAACAAAGTTACATATGGAATAATGCCCAAG 995  
 Db 318 AsnLysSerLysProTyrTyrThrGlyGluHisAlaLysAlaIleGlyAsnCysProIle 337  
 QY 996 TATATCAGCAAAACACACTTTAAAGCTGGCCTGAGGAGATATATACCAAGAAACGAA 1055  
 Db 338 TrpValLys---ThrProLeuLysLeuAlaAsnGlyThrLysTyrArgProProLalLys 356  
 QY 1056 ATC 1058  
 ;

Query Match:	20.55%	Indels:	220
DB:	9	Gaps:	2
US-10-826-929A-1 (1-1061) x US-09-918-568-58 (1-347)			
QY	30	ATGAGACACACCAATTTTTCATCTACTACTACCCATTTGGTCTACAGTCAAAAC---CCA	86
DB	1	MetLysThrIleAlaLeuSerTyrIlePheCysLeuAlaLeuGlyGlnAspLeuPro	20
QY	87	ACCACTGGAAACACACAGCACCATTTATGCTCTGGGACACCATCGCATAGCAATGAACA	146
DB	21	GlyAsnAspAsnSerThrAlaThrLeuCysLeuGlyHisAlaValProAsnGlyThr	40
QY	147	TTGTAAAAACATAACTAGATGACCCAAATTTGAGGTGACAAATGCTACTGAATTTAGTTCAG	206
DB	41	LeuValLysThrIleThrAspAspGlnIleLeuValThrAsnAlaThrGluLeuValGln	60
QY	207	AGCATTTCAATAGGAAATATCAACAACCTCATATAAAGTTCTAGATGGAATAATTCG	266
DB	61	SerSerSerThrGlyLysIleCysAsnAsn-----	70
QY	267	ACATTAATAGATGAATGCTAGGAGACCCCACTGTGATGTCTTCAGTATGAGAAATTCG	326
DB	70	-----	70
QY	327	GNCTCTTTCATGAAGAAGCAGCGCTTTTCAGCAATTTGCTACCCATATGACATCCCTGAC	386
DB	70	-----	70
QY	387	TATGATCGCTCCGGTCCATTGTAGCATCTCAGAACATTTAGAAATTCACAGCAGGGA	446
DB	70	-----	70
QY	447	TTACATGGACAGGTGTCACTCAAAACGGAAGATGGAGCCTGCAAAAGGGGATCAGCC	506
DB	70	-----	70
QY	507	GATAGTTTCTTTAGCCGACTGAATTTGGCTAAACAAATCTGAAACTCTTAACCCACATTCG	566
DB	70	-----	70
QY	567	ATGTGCAATGCTCAACAATAAAATTTTCGAACTATACATCTGCGGGGATTCATCAC	626
DB	70	-----	70
QY	627	COGAGCTTCAACCAACAGCAGACAGATTTGTATCCAAAGATTCAGCAGAGTAACAGTC	686
DB	70	-----	70
QY	687	TCACAAAAAGAGTCAACAAACGATAGTCCCTTAATATCGGATCTAGACCGTGGGTAGG	746
DB	70	-----	70
QY	747	GGTCAATCAGCAGGATTAAGCATATATCTGGACCATTTGTAAACCTGGAGATATCTAATG	806
DB	70	-----	70
QY	807	ATAACAGTAATGCGCACTTAGTTGTCACCGGGGATATTTTAAATTTGAAACAGGGA	866
DB	70	-----	70
QY	867	AGCTCTTAATGAGATCAGATGCACCCATAGACATTTGTCTGAATGTATTATACCA	926
DB	71	-----IleAspThrCysIleSerGluCysIleThrPro	81
QY	927	AATGGAAGCATCCCCACGACCAACCATTTTCAAAATGTGAACAAAGTTACATATGAAAA	986
DB	82	AsnGlySerIleProAsnAspLysProPheGlnAsnValAsnLysIleThrTyrGlyAla	101
QY	987	TGCCCAAGTATATCAGCGCAAAACATTTTAAAGCTGGCCATCGGATGAGGAATATACCA	1046
DB	102	CysProLysTyrValLysGlnAsnThrLeuLysLeuAlaThrGlyMetAsnValPro	121



```
/ NUMBER OF SEQ ID NOS: 3484
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 3466
/ LENGTH: 412
/ TYPE: PRT
/ ORGANISM: Influenza A virus
US-10-224-999A-3466

Alignment Scores:
Pred. No.: 1.69e-44 Length: 412
Score: 536.50 Matches: 123
Percent Similarity: 54.02% Conservative: 72
Best Local Similarity: 34.07% Mismatches: 145
Query Match: 28.06% Indels: 21
DB: 14 Gaps: 10

US-10-826-929A-1 (1-1061) x US-10-224-999A-3466 (1-412)
QY 6 AACGAGGGATATTTCTGTCATCATGAAGACACCAATTTTGTATCTACTGACCCAT 65
DB 2 LysAlaGlyVal-----ThrMetGluLysLeuIleValIleAlaMetLeu----- 17
QY 66 TGGGCTCTACAGTCAAAACCAACAGCTGGAACACACAGCCACCATTTATGCTGGACAC 125
DB 18 -----AlaSerThrAsnAlaTyrAspArgIleCysIleGlyTyr 30
QY 126 CATGCACTAGCAATGGAATGTTGTAATAAACAATTAATGATGACCAAAATGAGGTGACA 185
DB 31 GlnSerAsnAsnSerThrAspThrValAsnThrLeuIleGlnAsnValProValThr 50
QY 186 AATGCTACTGAATTAATGCTAGAGCAATTCATAGGGAATAATGCAACAACTCATATAA 245
DB 51 GlnThrMetGluLeuValGluThrGluLysHisProAlaTyrCysAsnThrAspLeuGly 70
QY 246 GTT---CTAGATGGAAGAAATTCACATTAATAGATGCAATGCTAGGAGACCCCACTGT 302
DB 71 AlaProLeuGluLeuArgAspCysIleGluAlaValIleTyrGlyAsnProLysCys 90
QY 303 GATGTC---TTCAGTATGGAATTTGGACCTCTTCATAGAAGAGCAGCGCTTTCAGC 359
DB 91 AspIleHisLeuLysAspGlnGlyTrpSerTyrIleValGluArgProSerAlaProGlu 110
QY 360 AAT---TGCTPACCATATGATCCCTGCTACTGATGCTCGCTGCTCCATTTAGCATCC 416
DB 111 GlyMetCysTyrProGlySerIleGluAsnLeuGluGluLeuArgPheValPheSerSer 130
QY 417 TCAGGAACATTAGAA---TTCACAGCAGAGGGATTCACATGGACAGGTGTCATCAAAAC 473
DB 131 AlaAlaSerTyrLysArgIleAlaGLeuPheAspTyr-SerArgTrpAsnValThrArgSer 150
QY 474 GGAAGAGTGGAGCTGCAAAAGGGATCA---GCCGATAGTTCTTTAGCCGACTGAAT 530
DB 151 GlyThrSerLysAlaCysAsnAlaSerThrGlyGlnSerPheTyrArgSerIleAsn 170
QY 531 TGGCTAACAA---AAATCTGGAATCTTACCCACATTTGAATGTGCAATGCTCAACAAT 587
DB 171 TrpLeuThrLysLysLysProAspThrTyrAspPheAsnGluGlyThrTyrValAsnAsn 190
QY 588 AAAAATTCGACAAACTATACATCTGGGGGATTCATCACCCGAGCTCAAAACCAACAGCAG 647
DB 191 GluAspGlyAspIleIlePheLeuTrpGlyIleHisHisProAspThrLysLysGluGln 210
QY 648 ACAGATTGTACATCCAGAAATCAGGACGAGTAAACAGTCTCAACAAAGAAAGTCAACAA 707
DB 211 ThrThrLeuTyrLysAsnAlaAsnThrLeuThrSerValThrThrAsnThrIleAsnArg 230
QY 708 ACGATAGTCCCTATATCGGATCTAGACCGTGGGTAGGGGTCAATCAGGAGGATGAAGC 767
DB 231 AsnPheGlnProAsnIleGlyProArgProLeuValArgGlyGlnGlnGlyArgMetAsp 250
QY 768 ATATCTGGACCAATGTAACCTGGAGATATCTTAATGATAACAGTAAATGCAACTTA 827
DB 251 TyrTyrTrpGlyIleLeuLysArgGlyGluThrLeuLysIleArgThrAsnGlyAsnLeu 270

828 GTTGACCGCGGGATATTTAAATTTGAAACAGGAAAGCTCT-----GTAATG 878
DB 271 IleAlaProGluPheGlyTyrLeuLeuLys---GlyGluSerHisGlyArgIleGln 289
QY 879 AGATCAGATGACCCATAGACATTTGTGTCTGAATGCTATATACCAACAAATGGAAGCATC 938
DB 290 AsnGluAspIleProIleGlyAsnCysAsnThrLysCysGlnThrTyrAlaGlyAlaIle 309
QY 939 CCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACATATGGAANAATGCCCAAGTAT 998
DB 310 AsnSerSerLysProPheGlnAsnAlaSerArgHisTyrMetGlyGluCysProLysTyr 329
QY 999 ATCAGGCAAAACACTTTAAAGCTGCCACTGGAGTGAAGAGAAATATACCAAGAAAGCAATC 1058
DB 330 ValLysLysAlaSerLeuArgLeuAlaValGlyLeuArgAsnThrProSerValGluPro 349
QY 1059 AGA 1061
DB 350 ARG 350

RESULT 9
US-10-381-530-12
/ Sequence 12, Application US/10381530
/ Publication No. US20040137013A1
/ GENERAL INFORMATION:
/ APPLICANT: KATINGER, Hermann
/ APPLICANT: EGOROV, Andre
/ APPLICANT: FERKO, Boris
/ APPLICANT: ROMANOVA, Julia
/ APPLICANT: KATINGER, Dietmar
/ TITLE OF INVENTION: LIVE VACCINE AND METHOD OF MANUFACTURE
/ FILE REFERENCE: P/167-134
/ CURRENT APPLICATION NUMBER: US/10/381,530
/ PRIOR FILING DATE: 2003-11-24
/ PRIOR APPLICATION NUMBER: PCT/EP01/11087
/ PRIOR FILING DATE: 2001-09-25
/ PRIOR APPLICATION NUMBER: 00120896.6
/ PRIOR FILING DATE: 2000-09-25
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 12
/ LENGTH: 562
/ TYPE: PRT
/ ORGANISM: Influenza virus A/Singapore/1/57/ca
US-10-381-530-12

Alignment Scores:
Pred. No.: 1.63e-42 Length: 562
Score: 517.00 Matches: 108
Percent Similarity: 52.01% Conservative: 60
Best Local Similarity: 33.44% Mismatches: 149
Query Match: 27.04% Indels: 6
DB: 16 Gaps: 5

US-10-826-929A-1 (1-1061) x US-10-381-530-12 (1-562)
QY 111 TTATGTCTGGGACACCATCGATGCAATGGAACATTCGTTAAACAAATAGTATGATGAC 170
DB 18 IleCysIleGlyTyrHisAlaAsnSerThrGluLysValAspThrIleLeuGln 37
QY 171 CAAATTTAGGTGACAAATGCTACTGAATTTAGTTCAGAGCATTTCAATAGGGAATATGTC 230
DB 38 AsnValThrValThrHisAlaLysAspIleLeuGluLysThrHisAsnGlyLysLeuCys 57
QY 231 AAC---AATCATATTAAGTTCTAGATGGAAGAAATTCACATTAATAGATCAATGCTA 287
DB 58 LysLeuAsnGlyIleProLeuGluLeuGlyAspCysSerIleAlaGlyTrpLeu 77
QY 288 GGAGACCCCACTGTGAT---GTCTCCAGTATGAGATTTGGACCTCTTCATAGAAAGA 344
DB 78 GlyAsnProGluCysAspArgLeuLeuSerValProGluTrpSerTyrIleMetGluLys 97
```

QY 690 ACAAAGAGTCAACAAACGATAGTCCCTATATCGGATAGACCGTGGGTAGGGGT 749  
 Db |||||  
 221 ThrLysArgSerGlnThrIleProAsnIleGlySerArgProArgValArgGly 240  
 QY |||||  
 750 CAATCAGGAGGATAGCATATCTGACCATTTGTAACCTGGAGATATCTATATGATA 809  
 Db |||||  
 241 GlnSerGlyArgIleSerIleThrIleValLysProGlyAspIleLeuMetIle 260  
 QY |||||  
 810 AACAGTAATGGCACTTAGTTGCACCGCGGGATATTTAAATTTGAAAACAGGAAAGC 869  
 Db |||||  
 261 AsnSerAsnGlyAsnLeuValAlaProArgGlyThrPheLysLeuLysThrGlyLysSer 280  
 QY |||||  
 870 TCTGTAATGAGATCAGATGACCATGACCATTTGTTGTTCTGTAATGTTATACCAAT 929  
 Db |||||  
 281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn 300  
 QY |||||  
 930 GGAAGCATCCCAACACCAACCATTTTCAAAATGTGAAACAAAGTTACATATGGAATGC 989  
 Db |||||  
 301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 320  
 QY |||||  
 990 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1049  
 Db |||||  
 321 ProLysIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu 340  
 QY |||||  
 1050 AAGCAATCAGA 1061  
 Db |||||  
 341 LysGlnIleArg 344

## RESULT 7

US-10-099-619-2  
 ; Sequence 2, Application US/10099619  
 ; Publication No. US20020168384A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CLAESSENS, JOHANNES AJ  
 ; APPLICANT: WALTER, FUCHS  
 ; TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS VACCINE  
 ; FILE REFERENCE: 2001001US  
 ; CURRENT APPLICATION NUMBER: US/10/099,619  
 ; PRIOR FILING DATE: 2002-03-15  
 ; PRIOR APPLICATION NUMBER: EP012009759  
 ; PRIOR FILING DATE: 2001-03-15  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 564  
 ; TYPE: PRN  
 ; ORGANISM: AVIAN INFLUENZA VIRUS  
 US-10-099-619-2

## Alignment Scores:

Pred. No.: 2,63e-55 Length: 564  
 Score: 645.00 Matches: 132  
 Percent Similarity: 57.56% Conservative: 66  
 Best Local Similarity: 38.37% Mismatches: 132  
 Query Match: 33.73% Indels: 14  
 DB: 13 Gaps: 7

US-10-826-929a-1 (1-1061) x US-10-099-619-2 (1-564)

QY 30 ATGAGACAAACCATTTTGTATCTACTGACCCCATTTGGTCTACAGTCAAAACCCAAACC 89  
 Db |||||  
 1 MetAsnThrGlnIleLeuValPheAlaLeuValAlaIle-----ProThr 16  
 QY 90 AGTGGNAACAACACACCCACATATGCTGGGACACCATGACAGTAGCAATGACATG 149  
 Db |||||  
 17 SerAlaAspLys-----IleCysLeuGlyHisAlaValSerAsnGlyThrLys 33  
 QY 150 GTAAAAACAATACTGATGACCAATTTGAGGTGACAAATGCTACTGTAATGTTCTCAGAGC 209  
 Db |||||  
 34 ValAsnThrLeuThrGluArgGlyValGluValAlaAsnAlaThrGluThrValGluArg 53  
 QY 210 ATTTCAATAGGAAATATGCAACATCTCATATAAAGTTCTAGATGGAAGAAATTCACA 269  
 Db |||||

Db 54 ThrAsnValProArgIleCysSerLysGlyLysArgThrValAspLeuGlyGlnCysGly 73  
 QY |||||  
 270 TTAATAGATGCATCTAGGACACCCCTAGTGTGATCTTCCAGTATGAGAAATGGGAC 329  
 Db |||||  
 74 LeuLeuGlyThrIleThrGlyProGlnCysAspGlnPheLeuGluPheSerAlaAsp 93  
 QY |||||  
 330 CTCCTCATAGAAAGACAGCGCTTTCAGCAATTTGCTACCATATGACATCCCTCCTCATAT 389  
 Db |||||  
 94 LeuIleIleGluArgArgGluCysSerAspValCysTyrProGlyLysPheValAsnGlu 113  
 QY |||||  
 330 GCATCGCTCCGGTCCATTGTAGCATCTCAGAAACATTAGAAATTCACAGCAGAGGATTC 449  
 Db |||||  
 114 GluAlaLeuArgGlnIleLeuArgGluSerGlyGlyIleAspLysGluAlaMetGlyPhe 133  
 QY |||||  
 450 ACATCGACAGGTGTCCTCACTCAAAACGAGAGAGTGGAGCTGCAAAAGGGATCAGCCGAT 509  
 Db |||||  
 134 ThrTyrSerGlyIleArgThrAsnGlyThrThrSerThrCysArgArg---SerGlySer 152  
 QY |||||  
 510 AGTTTCTTTAGCCGACTGAATTTGGCTAAACAAATCTGGAAC-----TCTTACCCCA 563  
 Db |||||  
 153 SerPheTyrAlaGluMetLysTrpLeuLeuSerAsnThrAspAsnAlaAlaPheProGln 172  
 QY |||||  
 564 TTGAATGTGACAAATGCCCTTAAACAAATTTTCGACAACTATACATCTGGGGATTCAT 623  
 Db |||||  
 173 MetThrLysSerTyrLysAsnThrArgLysAspProAlaLeuIleIleIleIleIleHis 192  
 QY |||||  
 624 CACCGAGCTCAACCAACACAGCAGCAATTTGATCATCCCAAGATCAGGACGAGTAAACA 683  
 Db |||||  
 193 HisSerGlySerThrThrGluGlnThrLysLeuTyrGlySerGlyAsnLysLeuIleThr 212  
 QY |||||  
 684 GTCTCAACAAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGTT 743  
 Db |||||  
 213 ValGlySerSerAsnTyrGlnGlnSerPheValProSerProGlyGluArgProGlnVal 232  
 QY |||||  
 744 AGGGTCAATCAGCAGGAGTAAGCATATATCTGGACCATTTGTAACCTGGAGATATCTCTA 803  
 Db |||||  
 233 AsnGlyGlnSerGlyArgIleAspPheHisIleTrpLeuMetLeuAsnProAsnAspThrVal 252  
 QY |||||  
 804 ATGATAACACAGTAAATGGCACTTAGTTGCACCG---CGGGGATATTTAAATTTGAAACA 860  
 Db |||||  
 253 ThrPheSerPheAsnGlyAlaPheIleAlaProAspArgAlaSerPhe-----LeuArg 270  
 QY |||||  
 861 GGGAAAAGCTCTGTAATGAGATCAGATCGACCCCATAGACATT---TGTGTCTCTCAATGT 917  
 Db |||||  
 271 GlyLysSerMetGlyIleGlnSerGlyValGlnValAspAlaAsnCysGluCysCys 290  
 QY |||||  
 918 ATTACCAAAATGGAAGCATCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACA 977  
 Db |||||  
 291 TyrHisSerGlyGlyThrIleIleSerAsnLeuProPheGlnAsnIleAsnSerArgAla 310  
 QY |||||  
 978 TATGGAAAATGCCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGG 1037  
 Db |||||  
 311 ValGlyLysCysProArgTyrValLysGlnGluSerLeuLeuAlaThrGlyMetLys 330  
 QY |||||  
 1038 AATATACAGAA 1049  
 Db |||||  
 331 AsnValProGlu 334

## RESULT 8

US-10-224-999A-3466  
 ; Sequence 3466, Application US/10224999A  
 ; Publication No. US20030171318A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Myriad Genetics, Inc.  
 ; APPLICANT: Morham, Scott  
 ; APPLICANT: Zavitz, Kenton  
 ; APPLICANT: Hobden, Adrian  
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
 ; FILE REFERENCE: 5004.01  
 ; CURRENT APPLICATION NUMBER: US/10/224,999A  
 ; PRIOR FILING DATE: 2003-03-03  
 ; PRIOR APPLICATION NUMBER: US 60/313,695  
 ; PRIOR FILING DATE: 2001-08-20

```
QY 90 AGTGGAAACACACACCCACATTTATGCTGGGACACACCTAGCAGTAATGGAATG 149
Db 21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40
QY 150 GTAAAAACAATACTCATGACCAAAATGAGGTGACAAATGCTACTGAATTTAGATTCAGAGC 209
Db 41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60
QY 210 ATTTCATAGGGAATAATGCAACAATCATATAAAGTTCTAGATGGAAGAAATTCACACA 269
Db 61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr 80
QY 270 TTAATGATGCAATGCTAGAGACCCCACTGATGCTCTCCAGTATGAGATTTGGGAC 329
Db 81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyrGluAsnTrpAsp 100
QY 330 CTCTTCATAGAAAGACGACGCTTTTCAGCAATTTGCTACCCATATGACATCCCTGACTAT 389
Db 101 LeuPheIleGluArgSerSerAlaPheSerSerCysTyrProTyrAspIleProAspTyr 120
QY 390 GCATCGCTCGTCCATTTAGCATCTCAGGAACAATTTAGAAATTCACAGAGGGATTC 449
Db 121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140
QY 450 ACATGACACGCTCTCACTCAAAACGGAAGTGGAGCCTGCAAAAGGGGATCCAGCCGAT 509
Db 141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlySerCysLysArgGlySerAlaAsp 160
QY 510 AGTTTCTTTAGCCGACTGTAATTCGCAAAATCTGGAACCTTTACCCCAATTTGAAT 569
Db 161 SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyrProThrLeuAsn 180
QY 570 GTGACAAATCCCTAACATATAAATTTTCGACAACTATACATCTGGGGGATTCATCCCG 629
Db 181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleTrpGlyIleHisHisPro 200
QY 630 AGCTCAAAACACACAGCAGACAGATTTGTATCATCCAAAGATCAGGACGAGTAACAGTCTCA 689
Db 201 SerSerAsnLysGluGlnThrLysLeuTyrIleGlnGluSerGlyArgValThrValSer 220
QY 690 ACAAAGAAGTCAACAACAGATAGTCCCTTAATATCGGATCTAGACCCGTGGGTAGGGGT 749
Db 221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProArgValArgGly 240
QY 750 CAATCAGCAGGATAGCATATACTGACCAATTTGTAACCTGAGATATCTTAATGATA 809
Db 241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle 260
QY 810 AACAGTAATGGCAACTTAGTTGACCCGGGGATATTTTAAATTTGAAACACAGGGAAGC 869
Db 261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuLysThrGlyLysSer 280
QY 870 TCTGTAATGAGATCAGATGACCCCATAGACATTTGTGTCTGAATGTATTACACCAAT 929
Db 281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn 300
QY 930 GGAAGCATCCCAACGACAAACCATTTCAAAATGTGAACAACTTACATATGGAATGTC 989
Db 301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 320
QY 990 CCCAAGTATATCAGGCAAAACACTTTTAAAGCTGGCCACTGGGATGAGGATATACAGAA 1049
Db 321 ProLysTyrIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu 340
QY 1050 AAGCAATCAGA 1061
Db 341 LysGlnIleArg 344
```

## RESULT 6

US-10-734-373-8

; Sequence 8, Application US/10734373

; Publication No. US20040137015A1

```
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/734,373
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-734-373-8
```

```
Alignment Scores:
Pred. No.: 1,98e-169 Length: 565
Score: 1787.00 Matches: 333
Percent Similarity: 99.42% Conservative: 9
Best Local Similarity: 96.80% Mismatches: 2
Query Match: 93.46% Indels: 0
DB: 16 Gaps: 0
```

US-10-826-929A-1 (1-1061) x US-10-734-373-8 (1-565)

```
QY 30 ATGAGACAAACCATTTATTTGATCTACTGACCCATTTGGTCTACAGTCAAAACCAAC 89
Db 1 MetLysThrThrIleIleLeuIleProLeuThrHisTrpValTyrSerGlnAsnProThr 20
QY 90 AGTGGAAACAACACAGCCACATTTATGCTGGGACACCATTCAGTACGAAATGGAATG 149
Db 21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40
QY 150 GTAAAAACAATAACTGATGACCAAAATTTGAGGTGACAAATGCTACTGAATTTAGTTCAGAGC 209
Db 41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60
QY 210 ATTTCATAGGGAATAATGCAACAATCATATAAAGTTCTAGATGGAAGAAATTCACACA 269
Db 61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr 80
QY 270 TTAATGATGCAATGCTAGAGACCCCACTGATGCTCTCCAGTATGAGATTTGGGAC 329
Db 81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyrGluAsnTrpAsp 100
QY 330 CTCTTCATAGAAAGACGACGCTTTTCAGCAATTTGCTACCCATATGACATCCCTGACTAT 389
Db 101 LeuPheIleGluArgSerSerAlaPheSerSerCysTyrProTyrAspIleProAspTyr 120
QY 390 GCATCGCTCGTCCATTTAGCATCTCAGGAACAATTTAGAAATTCACAGAGGGATTC 449
Db 121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140
QY 450 ACATGACACAGTGTCACTCAAAACGGAAGTGGAGCCTGCAAAAGGGGATCCAGCCGAT 509
Db 141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlySerCysLysArgGlySerAlaAsp 160
QY 510 AGTTTCTTTAGCCGACTGTAATTCGCAAAATCTGGAACCTTTACCCCAATTTGAAT 569
Db 161 SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyrProThrLeuAsn 180
QY 570 GTGACAAATCCCTAACATATAAATTTTCGACAACTATACATCTGGGGGATTCATCCCG 629
Db 181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleTrpGlyIleHisHisPro 200
QY 630 AGCTCAAAACACACAGCAGACAGATTTGTATCATCCAAAGATCAGGACGAGTAACAGTCTCA 689
Db 201 SerSerAsnLysGluGlnThrLysLeuTyrIleGlnGluSerGlyArgValThrValSer 220
```

```
Db 341 LysGlnIleArg 344
|||||
RESULT 4
US-10-065-133A-8
; Sequence 8, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-8
Alignment Scores:
Pred. No.: 1,98e-169 Length: 565
Score: 1787.00 Matches: 333
Percent Similarity: 99.42% Conservative: 9
Best Local Similarity: 96.80% Mismatches: 2
Query Match: 93.46% Indels: 0
DB: 14 Gaps: 0
US-10-826-929A-1 (1-1061) x US-10-065-133A-8 (1-565)
QY 30 ATGAAGACACCAATTATTTGATCTACTGACCCATTGGGTCTACAGTCAAAACCAACC 89
Db 1 MetLysThrThrIleLeuIleProLeuThrHisTrpValTy-SerGlnAsnProThr 20
QY 90 AGTGGAAACACACAGCCCATATGTCGGGACACCATGCGAGTACCAATGGACATTG 149
Db 21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40
QY 150 GTAAAAACAATACTGATGACCAAAATGAGTGACAAATGCTACTGAATTAGTTCAGAGC 209
Db 41 ValLysThrIleThrAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60
QY 210 ATTTCAATAGGAAATATGCAACAACTCATATAAAGTTCTAGATGGAGAAATTCGACA 269
Db 61 IleSerIleGlyLysIleCysAsnAsnSerTyArgValLeuAspGlyArgAsnCysThr 80
QY 270 TTAATAGATGCAATGCTAGGACACCCCACTGCTGCTCTCCAGTATGAGATTGGAC 329
Db 81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyGluAsnTrpAsp 100
QY 330 CTCCTTCATAGAAGACAGCGCTTTTCAGCAATTTGCTACCCATATGACATCCCTGACTAT 389
Db 101 LeuPheIleGluArgSerSerAlaPheSerSerCysTyProTyAspIleProAspTy 120
QY 390 GCATCGCTCCGTCCTATTCATCTCTCAGGAACATTAGAATTCACAGCAGGAGATTC 449
Db 121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140
QY 450 ACATGACAGGTGTCATCTAAACCGGAGAGTGGAGCCCTGCAAAAGGGGATCAGCCGAT 509
Db 141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlySerCysLeuArgGlySerAlaAsp 160
QY 510 AGTTTCTTTAGCGCACTGAATTTGGCTAAACAAATCTGGAATCTTACCCCACTTGAAT 569
Db 161 SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyProThrLeuAsn 180
QY 570 GTGACAATGCCCTAACAAATAAAATTTTCGACAAACTATACATCTGGGGGATTCATCACC 629
Db 181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyIleTrpGlyIleHisPro 200
QY 630 AGCTCAACACCAACAGCAGCAGAGATTGTACATCCAAAGATCAGGACGAGTACACTCTCA 689
Db 201 SerSerAsnLysGluGlnThrLysLeuTyIleGlnGluSerGlyArgValThrValSer 220
QY 690 ACAAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCCGTGGGTAGGGGT 749
Db 221 ThrLysArgSerGlnThrIleIleProAsnIleGlySerArgProArgValArgGly 240
QY 750 CAATCAGCAGGATAAGCATATATCTGACCACTTGTAAACCTGAGATATCTATATGATA 809
Db 241 GlnSerGlyArgIleSerIleTyTrpThrIleValLysProGlyAspIleLeuMetIle 260
QY 810 AACAGTAATGCAACTTAGTTCACCGCGGATATTTTAAATTCGAAACAGGGAAGAC 869
Db 261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyPheLysLeuLysThrGlyLysSer 280
QY 870 TCTGTAATGAGATCAGATGACCCATAGACATTTGTGTCTCTGAATGATTATACACAAAT 929
Db 281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn 300
QY 930 GGAAGCATCCCAACGACAAACCATTTTCAAAATGTGAACAAAGTTTACATATGGAATGC 989
Db 301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyGlyLysCys 320
QY 990 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1049
Db 321 ProLysTyIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu 340
QY 1050 AAGCAAAATCAGA 1061
Db 341 LysGlnIleArg 344
US-10-434-811A-8
; Sequence 8, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-434-811A-8
Alignment Scores:
Pred. No.: 1,98e-169 Length: 565
Score: 1787.00 Matches: 333
Percent Similarity: 99.42% Conservative: 9
Best Local Similarity: 96.80% Mismatches: 2
Query Match: 93.46% Indels: 0
DB: 15 Gaps: 0
US-10-826-929A-1 (1-1061) x US-10-434-811A-8 (1-565)
QY 30 ATGAAGACACCAATTATTTGATCTACTGACCCATTGGGTCTACAGTCAAAACCAACC 89
Db 1 MetLysThrThrIleLeuIleProLeuThrHisTrpValTy-SerGlnAsnProThr 20
QY 90 AGTGGAAACACACAGCCCATATGTCGGGACACCATGCGAGTACCAATGGACATTG 149
Db 21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40
QY 150 GTAAAAACAATACTGATGACCAAAATGAGTGACAAATGCTACTGAATTAGTTCAGAGC 209
Db 41 ValLysThrIleThrAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60
QY 210 ATTTCAATAGGAAATATGCAACAACTCATATAAAGTTCTAGATGGAGAAATTCGACA 269
Db 61 IleSerIleGlyLysIleCysAsnAsnSerTyArgValLeuAspGlyArgAsnCysThr 80
QY 270 TTAATAGATGCAATGCTAGGACACCCCACTGCTGCTCTCCAGTATGAGATTGGAC 329
Db 81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyGluAsnTrpAsp 100
QY 330 CTCCTTCATAGAAGACAGCGCTTTTCAGCAATTTGCTACCCATATGACATCCCTGACTAT 389
Db 101 LeuPheIleGluArgSerSerAlaPheSerSerCysTyProTyAspIleProAspTy 120
QY 390 GCATCGCTCCGTCCTATTCATCTCTCAGGAACATTAGAATTCACAGCAGGAGATTC 449
Db 121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140
QY 450 ACATGACAGGTGTCATCTAAACCGGAGAGTGGAGCCCTGCAAAAGGGGATCAGCCGAT 509
Db 141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlySerCysLeuArgGlySerAlaAsp 160
QY 510 AGTTTCTTTAGCGCACTGAATTTGGCTAAACAAATCTGGAATCTTACCCCACTTGAAT 569
Db 161 SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyProThrLeuAsn 180
QY 570 GTGACAATGCCCTAACAAATAAAATTTTCGACAAACTATACATCTGGGGGATTCATCACC 629
Db 181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyIleTrpGlyIleHisPro 200
QY 630 AGCTCAACACCAACAGCAGCAGAGATTGTACATCCAAAGATCAGGACGAGTACACTCTCA 689
Db 201 SerSerAsnLysGluGlnThrLysLeuTyIleGlnGluSerGlyArgValThrValSer 220
QY 690 ACAAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCCGTGGGTAGGGGT 749
Db 221 ThrLysArgSerGlnThrIleIleProAsnIleGlySerArgProArgValArgGly 240
QY 750 CAATCAGCAGGATAAGCATATATCTGACCACTTGTAAACCTGAGATATCTATATGATA 809
Db 241 GlnSerGlyArgIleSerIleTyTrpThrIleValLysProGlyAspIleLeuMetIle 260
QY 810 AACAGTAATGCAACTTAGTTCACCGCGGATATTTTAAATTCGAAACAGGGAAGAC 869
Db 261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyPheLysLeuLysThrGlyLysSer 280
QY 870 TCTGTAATGAGATCAGATGACCCATAGACATTTGTGTCTCTGAATGATTATACACAAAT 929
Db 281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn 300
QY 930 GGAAGCATCCCAACGACAAACCATTTTCAAAATGTGAACAAAGTTTACATATGGAATGC 989
Db 301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyGlyLysCys 320
QY 990 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1049
Db 321 ProLysTyIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu 340
QY 1050 AAGCAAAATCAGA 1061
Db 341 LysGlnIleArg 344
```

```
QY 450 ACATGGACAGGTGCTACTCAAAACGGAAGAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509
Db 141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlySerCysIysArgGluSerAlaAsp 160
QY 510 AGTTCTTTAGCCGACTGAATGGCTAAACAAATCTGGAAACTCTTACCCACATTTGAAT 569
Db 161 SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyrProThrLeuAsn 180
QY 570 GTGCAATCCTTAACAAATAAATTTTCGACAACTATACATCTGGGGGATTCATCACCCG 629
Db 181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleTrpGlyIleHisHisPro 200
QY 630 AGCTCAAAACCAACAGCAGACAGAAATGTATCATCCAAAGATCAGACGAGTAACAGTCTCA 689
Db 201 SerSerAsnLysGluGlnThrLysLeuTyrIleGlnGluSerGlyArgValThrValSer 220
QY 690 ACAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGGTAGGGGT 749
Db 221 ThrLysArgSerGlnGlnThrLysLeuTyrIleGlnGluSerGlyArgValThrValSer 240
QY 750 CAATCAGGAGGATAGCATATACATCGACCATTTGAAACCTGGAGATATCCTAATGATA 809
Db 241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuThrIle 260
QY 810 AACAGTAATGGCAACTTAGTTGACCGCGGGATATTTAAATTTGAAAACAGGAAAAGC 869
Db 261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuLysThrGlyLysSer 280
QY 870 TCTGTAATGAGATCAGATGACCCATAGACATTTGTGTCTGAATGTATTAACCAAT 929
Db 281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn 300
QY 930 GGAAGATCCCCAACACACAAACCATTTCAAAATGTCAACAAAGTTACATATGGAATGC 989
Db 301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 320
QY 990 CCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1049
Db 321 ProLysTyrIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu 340
QY 1050 AAGCAAAATCAGA 1061
Db 341 LysGlnIleArg 344
```

## RESULT 3

```
US-10-734-373-11
; Sequence 11, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/734, 373
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 565
; TYPE: PR1
; ORGANISM: Equine influenza virus H3N8
US-10-734-373-11
```

## Alignment Scores:

Pred. No.:	3,95e-170	Length:	565
Score:	1794.00	Matches:	333
Percent Similarity:	99.42%	Conservative:	9
Best Local Similarity:	96.80%	Mismatches:	2
Query Match:	93.83%	Indels:	0

```
DB: 16 Gaps: 0
US-10-826-929A-1 (1-1061) x US-10-734-373-11 (1-565)
QY 30 ATGAAGACACCACTTATTTTGTACTACTGACCCATTGGGTCTACAGTCAAAACCCCAACC 89
Db 1 MetLysThrThrIleLeuIleLeuLeuThrHisTrpValTyrSerGlnAsnProThr 20
QY 90 AGTGGAAAACAACACAGCCACATTTGTCTGGGACACCACCTGACAGTACCAATGAAACATTG 149
Db 21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40
QY 150 GTAAAAACAATACTGATGACCAAAATGAGGTGACAAATGCTACTGAAATAGTTTCAGAGC 209
Db 41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60
QY 210 ATTTCAATAGGAAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTCACAC 269
Db 61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr 80
QY 270 TTAATAGATGCAATGCTAGGACACCCCACTGTGTGTCTTCCAGTATGAGAATTCGGAC 329
Db 81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyrGlnAsnTrpAsp 100
QY 330 CTCCTCATAGAAAGACGACGCTTTTACAGCAATTCCTACCCATATGACATCCCTGACTAT 389
Db 101 LeuPheIleGluArgSerSerAlaPheSerSerCysTyrProTyrAspIleProAspTyr 120
QY 390 GCATGCTCCGTCATTTGTAGCATCTCAGGAACATTTAGAAATTCACAGCAGAGGATTC 449
Db 121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140
QY 450 ACATGACAGAGTGTCACTCAAAACGGAAGAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509
Db 141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlySerCysLysArgGluSerAlaAsp 160
QY 510 AGTTCTTTAGCGACTGAATTTGGTAAACAAATCTGGAACCTTTTACCCCACTTGAAT 569
Db 161 SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyrProThrLeuAsn 180
QY 570 GTGACATGCTTAAACATTAATAAATTTTCGACAACTATACATCTGGGGGATTCATCACCCG 629
Db 181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleTrpGlyIleHisHisPro 200
QY 630 AGCTCAAAACCAACAGCAGACAGAAATGTATCATCCAAAGATCAGACGAGTAAACAGTCTCA 689
Db 201 SerSerAsnLysGluGlnThrLysLeuTyrIleGlnGluSerGlyArgValThrValSer 220
QY 690 ACAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGGTAGGGGT 749
Db 221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProTrpValArgGly 240
QY 750 CAATCAGGAGGATAGCATATACATCGACCATTTGAAACCTGGAGATATCCTAATGATA 809
Db 241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuThrIle 260
QY 810 AACAGTAATGGCAACTTAGTTGACCGCGGGATATTTAAATTTGAAAACAGGAAAAGC 869
Db 261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuLysThrGlyLysSer 280
QY 870 TCTGTAATGAGATCAGATGACCCATAGACATTTGTGTCTGAATGTATTAACCAAT 929
Db 281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn 300
QY 930 GGAAGATCCCCAACACACAAACCATTTCAAAATGTCAACAAAGTTACATATGGAATGC 989
Db 301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 320
QY 990 CCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1049
Db 321 ProLysTyrIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu 340
QY 1050 AAGCAAAATCAGA 1061
```



GenCore version 5.1.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	
OM nucleic - protein search, using frame_plus_n2p model	
Run on: February 27, 2005, 18:32:14 ; Search time 157.5 Seconds (without alignments) 4419.749 Million cell updates/sec	
Title: US-10-826-929A-1	
Perfect score: 1912	
Sequence: 1 agcaaaagcaggggatattt.....taccagaaagcaaatcaga 1061	
Scoring table: BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	
Searched: 1385339 seqs, 328044528 residues	
Total number of hits satisfying chosen parameters: 2770678	
Minimum DB seq length: 0	
Maximum DB seq length: 2000000000	
Post-processing: Minimum Match 0%	
Maximum Match 100%	
Listing first 45 summaries	
Command line parameters:	
-MODEL=frame_n2p.model -DEV=xlp	
-Q=/cgn2_1/USPTO.spool_p/US10826929/runat_27022005_095245_27680/app_query.fasta_1.1223	
-DB=Published Applications AA -QWMT=fastan -SUFFIX=rapb -MINMATCH=0.1	
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62	
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100	
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0	
-MAXLEN=200000000 -USER=US10826929 -CGN_1_199 -runat_27022005_095245_27680	
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100	
-LONGLOG -DEV TIMEOUT=30 -WARN TIMEOUT=1 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5	
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7	
Database :	
Published Applications AA:	
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*	
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*	
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*	
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*	
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*	
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*	
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*	
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*	
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*	
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*	
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*	
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*	
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*	
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*	
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*	
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*	
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*	
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*	
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*	
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
SUMMARIES	
Result	Query
* US-10-065-133A-11	

No.	Score	Match	Length	DB	ID	Description
1	1794	93.8	565	14	US-10-065-133A-11	Sequence 11, Appl
2	1794	93.8	565	15	US-10-434-811A-11	Sequence 11, Appl
3	1794	93.8	565	16	US-10-734-373-11	Sequence 11, Appl
4	1787	93.5	565	14	US-10-065-133A-8	Sequence 8, Appl
5	1787	93.5	565	15	US-10-434-811A-8	Sequence 8, Appl
6	1787	93.5	565	16	US-10-734-373-8	Sequence 8, Appl
7	645	33.7	564	13	US-10-099-619-2	Sequence 2, Appl
8	536.5	28.1	412	14	US-10-224-939A-3466	Sequence 3466, Ap
9	517	27.0	562	16	US-10-381-530-12	Sequence 12, Appl
10	393	20.6	347	9	US-09-918-568-58	Sequence 58, Appl
11	225	11.8	47	14	US-10-105-232-283	Sequence 283, App
12	225	11.8	47	14	US-10-189-437-270	Sequence 270, App
13	222	11.6	584	16	US-10-381-530-30	Sequence 30, Appl
14	205	10.7	346	15	US-10-676-909-90	Sequence 90, Appl
15	184	9.6	39	14	US-10-105-232-284	Sequence 284, App
16	184	9.6	39	14	US-10-189-437-271	Sequence 271, App
17	177	9.3	348	9	US-09-918-568-50	Sequence 50, Appl
18	168	8.8	34	14	US-10-105-232-280	Sequence 280, App
19	158	8.8	34	14	US-10-189-437-267	Sequence 267, App
20	133	7.0	28	14	US-10-105-232-279	Sequence 279, App
21	133	7.0	28	14	US-10-189-437-266	Sequence 266, App
22	124	6.5	33	14	US-10-105-232-285	Sequence 285, App
23	124	6.5	33	14	US-10-189-437-272	Sequence 272, App
24	122	6.4	25	14	US-10-351-641-1063	Sequence 1063, Ap
25	118	6.2	24	13	US-10-044-034-11	Sequence 11, Appl
26	111.5	5.8	502	15	US-10-333-002-16	Sequence 16, Appl
27	109	5.7	23	13	US-10-044-034-3	Sequence 3, Appl
28	109	5.7	23	17	US-10-687-711-25	Sequence 25, Appl
29	108	5.6	55	14	US-10-105-232-208	Sequence 208, App
30	108	5.6	55	14	US-10-189-437-195	Sequence 195, App
31	107	5.6	956	13	US-10-121-032-63	Sequence 63, Appl
32	107	5.6	956	14	US-10-093-037-63	Sequence 63, Appl
33	106	5.5	232	15	US-10-381-770-12	Sequence 12, Appl
34	105	5.5	449	14	US-10-017-161-2108	Sequence 2108, Ap
35	105	5.5	449	15	US-10-292-798-1754	Sequence 1754, Ap
36	105	5.5	730	15	US-10-282-122A-57869	Sequence 57869, A
37	102	5.3	23	17	US-10-687-711-26	Sequence 26, Appl
38	102	5.3	49	14	US-10-105-232-274	Sequence 274, App
39	102	5.3	49	14	US-10-189-437-261	Sequence 261, App
40	99.5	5.2	802	16	US-10-437-963-160168	Sequence 160168,
41	98.5	5.2	402	15	US-10-425-114-68074	Sequence 68074, A
42	98	5.1	1459	15	US-10-369-493-6418	Sequence 6418, Ap
43	97.5	5.1	1180	14	US-10-193-764-61	Sequence 61, Appl
44	97.5	5.1	1188	14	US-10-193-764-59	Sequence 59, Appl
45	97	5.1	1041	9	US-09-042-488B-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1  
US-10-065-133A-11  
; Sequence 11, Application US/10065133A  
; Publication No. US20030199074A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/065,133A  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 565  
; TYPE: PRT  
; ORGANISM: Equine influenza virus H3N8  
US-10-065-133A-11

**This Page Blank (uspto)**



CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Patrea L. Pabst  
 STREET: 2800 One Atlantic Center  
 STREET: 1201 West Peachtree Street  
 CITY: Atlanta  
 STATE: GA  
 COUNTRY: USA  
 ZIP: 30309-3450  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/169,027  
 FILING DATE:

CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/453,848  
 FILING DATE: 30-MAY-1995  
 APPLICATION NUMBER: 08/120,607  
 FILING DATE: 13-SEP-1993  
 ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patrea L.  
 REGISTRATION NUMBER: 31,284  
 REFERENCE/DOCKET NUMBER: MGS101CIP  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (404)-873-8794

TELEFAX: (404)-873-8795

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 571 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

ORGANISM: Influenza virus

INDIVIDUAL ISOLATE: A/Shandong/9/93 rHA

FEATURE:

NAME/KEY: AcNPV 61K protein signal sequence

LOCATION: 1 to 18

FEATURE:

NAME/KEY: mature rHA

LOCATION: 19 to 553

US-09-169-027-15

Alignment Scores:  
 Pred. No.: 2,02e-139 Length: 571  
 Score: 1404.50 Matches: 253  
 Percent Similarity: 86.73% Conservative: 41  
 Best Local Similarity: 74.63% Mismatches: 44  
 Query Match: 73.46% Indels: 1  
 DB: 3 Gaps: 1

US-10-826-929A-1 (1-1061) x US-09-169-027-15 (1-571)

QY 48 TTGATACTACTGACCCATGGGTCTACAGTCAAAAC---CCAAACGAGTGGAAACAAACACA 104  
 Db 12 LeuValAlaValSerAsnAlaIleProGlyGlnAspLeuProGlyAsnAspAsnSerThr 31  
 QY 105 GCCACATATCTCTGGGACACCATGAGTACAGTACAAATGGAAACATTGGTAAACAACTACT 164  
 Db 32 AlaThrLeuCysLeuGlyHisHisAlaValProAsnGlyThrLeuValLysThrIleThr 51  
 QY 165 GATGACCAAAATGAGTGCAAAATGCTACTGATTAATAGTTAGTTCAGACGATTTCAATAGGAAA 224  
 Db 52 AsnAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSerSerThrGlyArg 71  
 QY 225 ATATGCAACAACACTCATATAAAGTTCTAGATGGAAGAAATTCACATTAATAGATGCAATG 284

Db 72 IleCysGlySerProHisArgIleLeuAspGlyLysAsnCysThrLeuIleAspAlaLeu 91  
 QY 285 CTAGAGAGACCCCATGCTGATGCTCTCCAGTATGAGAAATTCGGACCTCTTCATAGAAAGA 344  
 Db 92 LeuGlyAspProHisCysAspGlyPheGlnAsnLysGluTrpAspLeuPheValGluArg 111  
 QY 345 AGCAGCGCTTTTCAGCAATTTGCTACCATATGACATCCCTGATATGCTATGCTCGTCGGTCC 404  
 Db 112 SerLysAlaValSerAsnCysValProLysAspValProAspTyrAlaSerLeuArgSer 131  
 QY 405 ATTGATGATCTCTAGGAAACATTAGAAATTCACAGCAGAGGAGATTTCACATGGACAGGTGC 464  
 Db 132 LeuValAlaSerSerGlyThrLeuGluPheIleAsnGluAspPheAsnThrThrGlyVal 151  
 QY 465 ACTCAAAACGGAGAAGTGGAGCTGCAAAAGGGGATCAGCCGATAGTTCTTTTACCGCA 524  
 Db 152 AlaGlnAspGlyGlySerTyrAlaCysLysArgGlySerValAsnSerPheSerArg 171  
 QY 525 CTGAATTTGGCTAAACAAAATCTGGAACCTCTTACCCCAACATTCGAATGTGACATGCTAAC 584  
 Db 172 LeuAsnTrpLeuHisLysLeuGluTyrLysTyrProAlaLeuAsnValThrMetProAsn 191  
 QY 585 AATAAAATTTTCGACAAACTATACATCTGGGGGATTCATCCCCGAGTCAAAACCAACAG 644  
 Db 192 AsnGlyLysPheAspLysLeuTyrIleTrpGlyValHisPheProSerThrAspSerAsp 211  
 QY 645 CAGACAGAAATTTGATACATCCAGNAATCAGGACGAGTAACAGTCTCAACAAAGAGATGCA 704  
 Db 212 GlnThrSerLeuTyrValArgAlaSerGlyArgValThrValSerThrLysArgSerGln 231  
 QY 705 CAACGATAGTCCCTTAATATCGGATCTAGACCGTGGTGTAGGGGTCAATCAGGCAGGATA 764  
 Db 232 GlnThrValThrProAsnIleGlySerArgProTrpValArgGlyGlnSerSerArgIle 251  
 QY 765 AGCATATATCTGGACCATTTGATAACCTCGAGATATCTTAATGATATAACAGTAATGGCAAC 824  
 Db 252 SerIleTyrTrpThrIleValLysProGlyAspIleLeuLeuIleAspSerThrGlyAsn 271  
 QY 825 TTAGTTGACCGCGGGGATATTTAAATTTAAACAGGAGAAAGCTCTGTAATGATGATCA 884  
 Db 272 LeuIleAlaProArgGlyTyrPheLysIleArgAsnGlyLysSerSerIleMetArgSer 291  
 QY 885 GATGACCCCATAGACATTTGTGTCTCAATGTATTACACAAATGGAAGCATCCCAAC 944  
 Db 292 AspAlaProIleGlyAsnCysSerSerGluCysIleThrProAsnGlySerIleProAsn 311  
 QY 945 GACAAACCATTTCAAAATGTGAACAAAGTTACATATGGAATAATGCCCAAGTATATCAGG 1004  
 Db 312 AspLysProPheGlnAsnValAsnArgIleThrTyrGlyAlaCysProArgTyrValLys 331  
 QY 1005 CAAACACACTTTAAAGCTGCCCATCTGGGATGAGGATATACCAAGAAACCAATCAGA 1061  
 Db 332 GlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGluLysGlnThrArg 350

RESULT 15  
 US-08-453-848-21  
 ; Sequence 21, Application US/08453848  
 ; Patent No. 5858368  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Smith, Gale Eugene  
 ; APPLICANT: Volnovitz, Franklin  
 ; APPLICANT: Wilkinson, Bethanie Bident  
 ; APPLICANT: Voznesensky, Andrei I.  
 ; APPLICANT: Hackett, Craig Stanway  
 ; TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA  
 ; TITLE OF INVENTION: HEMAGGLUTININ MULTIVALENT VACCINES  
 ; NUMBER OF SEQUENCES: 31  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Patrea L. Pabst  
 ; STREET: 2800 One Atlantic Center  
 ; STREET: 1201 West Peachtree Street  
 ; CITY: Atlanta

APPLICANT: Wilkinson, Bethanie Eident  
APPLICANT: Voznesensky, Andrei I.  
APPLICANT: Hackett, Craig Stanway  
TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA  
TITLE OF INVENTION: HEMAGGLUTININ MULTIVALENT VACCINES  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Patrea L. Pabst  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM: disk  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/453,848  
FILING DATE: 30-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/120,607  
FILING DATE: 13-SEPT-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: MGS101CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-873-8794  
TELEFAX: (404)-873-8795  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 571 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Influenza virus  
INDIVIDUAL ISOLATE: A/Shandong/9/93 rHA  
FEATURE:  
NAME/KEY: ACNPV 61K protein signal sequence  
LOCATION: 1 to 18  
FEATURE:  
NAME/KEY: mature rHA  
LOCATION: 19 to 553  
US-08-453-848-15

Alignment Scores:  
Pred. No.: 2,02e-139 Length: 571  
Score: 1404.50 Matches: 253  
Percent Similarity: 86.73% Conservative: 41  
Best Local Similarity: 74.63% Mismatches: 44  
Query Match: 73.46% Indels: 1  
DB: 2 Gaps: 1

US-10-826-929A-1 (1-1061) x US-08-453-848-15 (1-571)

QY 48 TTGATACTACTGACCCATTGGGTCTACAGTCAAAAC---CCAAACAGTGGAAACACACA 104  
Db 12 LeuValAlaValSerAsnAlaIleProGlyGlnAspLeuProGlyAsnAspAsnSerThr 31  
QY 105 GCCAATTATGCTGGACACCATGCACTAGCAATGGACATGGTAAACAACTA 164  
Db 32 AlaThrLeuCysLeuGlyHisHisAlaValProAsnGlyThrLeuValIleThr 51

QY 165 GATGACCAAAATTGAGTGACAAATGCTACTGAATAGTTTACAGACATTTCAATAGGAAA 224  
Db 52 AsnAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSerSerThrGlyArg 71  
QY 225 ATATGCAACAACATCATATATAAGTTCTAGATGGAAGAAATTCACATATATAGATGCAATG 284  
Db 72 IleCysGlySerProHisArgIleLeuAspGlyLysAsnCysThrLeuIleAspAlaLeu 91  
QY 285 CTAGGAGACCCCTGCTGATGCTCTCCAGTATGAGAATGGGACCTCTTCATAGAAAGA 344  
Db 92 LeuGlyAspProHisCysAspGlyPheGlnAsnLysGluTrpAspLeuPheValGluArg 111  
QY 345 AGCAGCGCTTTCAGCAATTTGCTACCATATGACATCCCTGACTATGATCGCTCCGCTCC 404  
Db 112 SerLysAlaIleSerAsnCysTyrProTyrAspValProAspTyrAlaSerLeuArgSer 131  
QY 405 ATTGATGATCTCTCAGGAACATTAGAAATTCACAGCAGGAGGATTCATGAGCAGGTGTC 464  
Db 132 LeuValAlaSerSerGlyThrLeuGluPheIleAsnGluAspPheAsnTrpThrGlyVal 151  
QY 465 ACTCAAAACGGAAGAGTGGAGCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGA 524  
Db 152 AlaGlnAspGlyGlySerTyrAlaCysLysArgGlySerValAsnSerPhePheSerArg 171  
QY 525 CTGAATTTGGCTAAACAAATCTCGAAACTCTTACCCCACTTGAATGTGACAAATGCCTAAC 584  
Db 172 LeuAsnTrpLeuHisLysLeuGluTyrLysTyrProAlaLeuAsnValThrMetProAsn 191  
QY 585 AATAAAATTTGACAACTATACATCTGGGGGATTCATCCCGAGCTCAACACCAACAG 644  
Db 192 AsnGlyLysPheAspLysLeuTyrIleTrpGlyValHisIleProSerThrAspSerArg 211  
QY 645 CAGACAGAAATTCATCATCAAGCAGCAGTAAACAGTCTCAACAAAGAAAGTCAA 704  
Db 212 GlnThrSerLeuTyrValArgAlaSerGlyArgValThrValSerThrLysArgSerGln 231  
QY 705 CAAACGATAGTCCCTAAATATCGGATCTAGACCGTGGTTAGGGTCAATCAGCAGGATA 764  
Db 232 GlnThrValThrProAsnIleGlySerArgProTyrValArgGlyGlnSerSerArgIle 251  
QY 765 AGCATATCTGACCATTTGATAAACTGGAGATATCTTAATGATAAACAGTAAATGCAAC 824  
Db 252 SerIleTyrTrpThrIleValLysProGlyAspIleLeuLeuIleAspSerThrGlyAsn 271  
QY 825 TTAGTTGACCGCGGGATATTTAAATGAAACAGGAGAAAGCTCTCTAATGAGATCA 884  
Db 272 LeuIleAlaProArgGlyTyrPheLysIleArgAsnGlyLysSerIleMetArgSer 291  
QY 885 GATGACCCCATAGACATTTGTGTCTGAATGTATTACACCAAAATGGAAGCATCCCAAC 944  
Db 292 AspAlaProIleGlyAsnCysSerSerGluCysIleThrProAsnGlySerIleProAsn 311  
QY 945 GACAAACCATTTCAAATGTGAACAAAGTTACATATGGAATAATGCCCAAGTATATCAGG 1004  
Db 312 AspLysProPheGlnAsnValAsnArgIleThrTyrGlyAlaCysProArgTyrValLys 331  
QY 1005 CAAACACCTTTAAAGCTGCCACTGGATGAGGAATATACCAAGAAAGCAATATCACA 1061  
Db 332 GlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGluLysGlnThrArg 350  
RESULT 14  
US-09-169-027-15  
Sequence 15, Application US/09169027  
Patent No. 6245532  
GENERAL INFORMATION:  
APPLICANT: Smith, Gale Eugene  
APPLICANT: Volnovitz, Franklin  
APPLICANT: Wilkinson, Bethanie Eident  
APPLICANT: Voznesensky, Andrei I.  
APPLICANT: Hackett, Craig Stanway  
TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA  
TITLE OF INVENTION: HEMAGGLUTININ MULTIVALENT VACCINES  
NUMBER OF SEQUENCES: 31



```

QY      1047 GAAAGCAATCAGA 1061
      ||||||| |||
Db      341 GIuLySGlnThrArg 345

RESULT 11
US-08-453-848-7
; Sequence 7, Application US/08453848
; Patent No. 5898368
; GENERAL INFORMATION:
; APPLICANT: Smith, Gale Eugene
; APPLICANT: Volvovitz, Franklin
; APPLICANT: Wilkinson, Bethanie Eident
; APPLICANT: Voznesensky, Andrei I.
; APPLICANT: Hackett, Craig Stanway
; TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA
; TITLE OF INVENTION: HEMAGGLUTININ MULTIVALENT VACCINES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,848
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/120,607
; FILING DATE: 13-SEPT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MGS101CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 570 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Influenza virus
; INDIVIDUAL ISOLATE: A/Beijing/32/92 rHA
; FEATURE:
; NAME/KEY: AcNPV 61K protein signal sequence
; LOCATION: 1 to 18
; FEATURE:
; NAME/KEY: mature rHA
; LOCATION: 19 to 552
; US-08-453-848-7

Alignment Scores:
Pred. No.: 3 67e-141 Length: 570
Score: 1421.00 Matches: 254
Percent Similarity: 87.28% Conservative: 41
Best Local Similarity: 75.15% Mismatches: 43
Query Match: 74.32% Indels: 0
DB: 2 Gaps: 0

```

Db 161 SerGlyPhePheSerArgLeuAsnTrpLeuTyrLysSerGlyAsnThrTyrProMetLeu 180  
QY 567 ATGTGCAATGCTTAAACAAATTTTCGCAAACTATACATCTGGGGATTCATCAC 626  
Db 181 AsnValThrMetProAsnSerAspAsnPheAspLysLeuTyrTrpGlyValHis 200  
QY 627 CCGAGCTCAAAACCAACAGCAGACAGAAATGTACATCCCAAGATCAGGACGAGTAACAGTC 686  
Db 201 ProSerThrAspArgGluGlnThrAsnLeuTyrValGlnValSerGlyLysAlaThrVal 220  
QY 687 TCACAAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGGTAGG 746  
Db 221 PheThrLysArgSerGlnGlnThrIleProAsnSerArgSerArgProTrpValArg 240  
QY 747 GGTCAATCAGGAGGATAGCATATCTAGTGCACCGCGGGATATTTTAAATTTGAAAAACAGGAAA 806  
Db 241 GlyLeuSerSerArgLysIleStrThrIleValLysProGlyAspIleLeuIle 260  
QY 807 ATAAACAGTAATGCGCAACTTAGTGCACCGCGGGATATTTTAAATTTGAAAAACAGGAAA 866  
Db 261 IleAsnSerAsnGlyAsnLeuIleAlaProArgGlyTyrPheLysMetHisAsnGlyArg 280  
QY 867 ACCTGTGTAATGAGATCAGATCGACCCATAGACATTTGTGTCTGTGAATGTATACACA 926  
Db 281 SerSerIleMetArgSerAspAlaProIleGlyThrCysSerSerGluCysIleThrPro 300  
QY 927 ATGGAAGCATCCCAACGACAAACCTTTTAAAGCTGGCCACCTGGGATGAGGATATACCA 986  
Db 301 AsnGlySerIleProAsnAspLysProPheGlnAsnValAsnLysIleThrTyrGlyAla 320  
QY 987 TGCCCCAAGTATATCAGGCAAAACACTTTTAAAGCTGGCCACCTGGGATGAGGATATACCA 1046  
Db 321 CysProLysTyrValLysGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnIlePro 340  
QY 1047 GAAAGCAAAATCAGA 1061  
Db 341 GluLysGlnThrArg 345

RESULT 10  
US-09-784-984B-53  
; Sequence 53, Application US/09784984B  
; Patent No. 6576243  
; GENERAL INFORMATION:  
; APPLICANT: Merial Ltd.  
; APPLICANT: Audonnet, Jean-Christophe  
; APPLICANT: Bouchardon, Annabelle  
; APPLICANT: Baudu, Philippe  
; APPLICANT: Riviere, Michael  
; TITLE OF INVENTION: Polynucleotide Vaccine Formula Against Porcine Reproductive and  
; TITLE OF INVENTION: Respiratory Pathologies  
; FILE REFERENCE: 454313-2230.1  
; CURRENT APPLICATION NUMBER: US/09/784,984B  
; CURRENT FILING DATE: 2001-02-16  
; PRIOR APPLICATION NUMBER: FR 96/09338  
; PRIOR FILING DATE: 1996-07-19  
; PRIOR APPLICATION NUMBER: PCT/FR97/01313  
; PRIOR FILING DATE: 1997-07-15  
; PRIOR APPLICATION NUMBER: US 6,207,165  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 53  
; LENGTH: 566  
; TYPE: PRT  
; ORGANISM: Swine Influenza Virus  
US-09-784-984B-53

Alignment Scores:  
Pred. No.: 7,55e-142 Length: 566  
Score: 1427.50 Matches: 262  
Percent Similarity: 85.51% Conservative: 33  
Best Local Similarity: 75.94% Mismatches: 49

Query Match: 74.66% Indels: 1  
DB: 4 Gaps: 1  
US-10-826-929A-1 (1-1061) x US-09-784-984B-53 (1-566)  
QY 30 ATGAAGCAACCATATTTTGTATCTACTGACCCATCTGGGTCTACAGTCAAAAC---CCA 86  
Db 1 MetLysThrValIleAlaLeuSerTyrIlePheCysLeuValLeuGlyGlnAspLeuPro 20  
QY 87 ACCAGTGAACACACACAGCCACATATTATGTCCTGGGACACCATGAGTAGCAAAATGGAACA 146  
Db 21 GluAsnGlySerSerThrAlaLysProGlyLeuGlyHisHisAlaValProAsnGlyThr 40  
QY 147 TTGTGTAACAACTGATGACCAAAATTCAGGTGACAAATGCTACTGAAATAGTTTCTAG 206  
Db 41 LeuValLysThrIleThrAsnAspGlnIleGluValThrAsnAlaThrGluLeuValGln 60  
QY 207 AGCATTTCAATAGGAAAAATATGCAACACTCATATATAAGTTCTAGATGGAGAAATGTC 266  
Db 61 SerPheSerMetGlyLysIleCysAsnAsnProHisArgValLeuAspGlyAlaAsnCys 80  
QY 267 ACATTATAGATGCAATGCTAGGAGACCCCTGATGCTCTCCAGTATGAGAAATGG 326  
Db 81 ThrLeuIleAspAlaLeuLeuGlyAspProHisCysAspGlyPheGlnAsnGlnLysTrp 100  
QY 327 GACCTCTTCATAGAAAAGAGCAGCGCTTTACGCAATTCCTACCCATATGACATCCCTGAC 386  
Db 101 AspLeuPheValGluArgSerLysCysPheSerAsnCysTyrProTyrAspValProAsp 120  
QY 387 TATGATCGCTCCCGTCCATTTGATGATCTCTCAGAACATTAAGATTCAGAGAGGGA 446  
Db 121 TyrAlaSerLeuArgSerLeuIleAlaSerSerGlyThrLeuGluPheIleAsnGly 140  
QY 447 TTCATGAGCAGCTGCTCCTCAAAACGAGAGAGTGGAGCTCCAAAGGGGATCAGCC 506  
Db 141 PheAsnTrpThrGlyValThrGlnAsnGlyGlySerAsnAlaCysLysArgGlyProAsp 160  
QY 507 GATAGTTTCTTTAGCCGACTGAATTTGGCTAAACAAATCTGAAATCTTATCCCACTTG 566  
Db 161 SerGlyPhePheSerArgLeuAsnTrpLeuTyrLysSerGlyAsnThrTyrProMetLeu 180  
QY 567 AATGTGCAATGCTTAAACAAATAAATTTTCGCAAACTATATCATCTGGGGATTCATCAC 626  
Db 181 AsnValThrMetProAsnSerAspAsnPheAspLysLeuTyrIleTrpGlyValHis 200  
QY 627 CCGAGCTCAAAACCAACAGCAGACAGAAATGTACATCCCAAGATCAGGACGAGTAACAGTC 686  
Db 201 ProSerThrAspArgGluGlnThrAsnLeuTyrValGlnValSerGlyLysAlaThrVal 220  
QY 687 TCACAAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGGTAGG 746  
Db 221 PheThrLysArgSerGlnGlnThrIleProAsnSerArgSerArgProTrpValArg 240  
QY 747 GGTCAATCAGGAGGATAGCATATCTAGTGCACCGGTAGTAAACCTGGGAGATATCTAATG 806  
Db 241 GlyLeuSerSerArgLysIleStrThrIleValLysProGlyAspIleLeuIle 260  
QY 807 ATAAACAGTATGCAACTTAGTGCACCGCGGGATATTTTAAATTTGAAAAACAGGAAA 866  
Db 261 IleAsnSerAsnGlyAsnLeuIleAlaProArgGlyTyrPheLysMetHisAsnGlyArg 280  
QY 867 AGCTCTGTAATGAGATCAGATCGACCCATAGACATTTGTGTCTGTGAATGTATACACA 926  
Db 281 SerSerIleMetArgSerAspAlaProIleGlyThrCysSerSerGluCysIleThrPro 300  
QY 927 AATGGAAGCATCCCAACGACAAACACTTTTAAAGCTGGCCACCTGGGATGAGGATATACCA 986  
Db 301 AsnGlySerIleProAsnAspLysProPheGlnAsnValAsnLysIleThrTyrGlyAla 320  
QY 987 TGCCCCAAGTATATCAGGCAAAACACTTTTAAAGCTGGCCACCTGGGATGAGGATATACCA 1046  
Db 321 CysProLysTyrValLysGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnIlePro 340

US-10-434-811A-8  
Alignment Scores:  
Pred. No.: 8,75e-180 Length: 565  
Score: 1787.00 Matches: 333  
Percent Similarity: 99.42% Conservative: 9  
Best Local Similarity: 96.80% Mismatches: 2  
Query Match: 93.46% Indels: 0  
DB: 4 Gaps: 0

US-10-826-929A-1 (1-1061) x US-10-434-811A-8 (1-565)

QY 30 ATGAGACACACCATTTTGTACTACTACCTGAGCCCTTGTCTACAGTCAAAACCAAC 89  
Db 1 MetLysThrThrIleLeuLeuProLeuThrHisTrpValSerGlnAsnProThr 20  
QY 90 AGTGGAAACACACACCATTTATGCTGGGACACCATGCTAGTACCAATGGAACATG 149  
Db 21 SerGlyAsnAsnThrAlaThrLeuGlyLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40  
QY 150 GTAAAAACAATACATGACCAAAATGAGGTGACAAATGCTACTGAAATAGTTCAGAC 209  
Db 41 ValLysThrIleThrAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60  
QY 210 ATTTCAATAGGAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATGCACA 269  
Db 61 IleSerIleGlyLysIleCysAsnAsnSerTyArgValLeuAspGlyArgAsnCysThr 80  
QY 270 TTAATAGATGCAATGCTAGGAGACCCCTGCTGTGATGCTTCCAGTATGAGAAATGGGAC 329  
Db 81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnIleThrGluAsnTrpAsp 100  
QY 330 CTCTTCATGAGAAGACGCGCTTTTACGAATGCTACCATATGACATCCCTGACTAT 389  
Db 101 LeuPheIleGluArgSerAlaPheSerCysTyProTyArgSerIleProAspTy 120  
QY 390 GCATCGCTCGGTCCTATGATGCTCTCAGGAACATTAAGATTCACAGCAGGAGATTC 449  
Db 121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140  
QY 450 ACTGACAGCTGCTACTCAAAACGGAAGAGTGGAGCTGCAAAAGGGGATCAGCCGAT 509  
Db 141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlySerCysLysArgGlySerAlaAsp 160  
QY 510 AGTTCTTTAGCGACTGATGGCTTAAACAAATCTGGAACCTCTTACCCCACTTGAAT 569  
Db 161 SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyProThrLeuAsn 180  
QY 570 GTCACATGCTAAACAAATTTTCGACAACTATACATCTGGGGGATTCATCACCCG 629  
Db 181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyIleTrpGlyIleHisHisPro 200  
QY 630 AGTCAAAACCAACAGCAGACAGAAATGTACATCAAGAAATCAGGACGAGTAACAGTCTCA 689  
Db 201 SerSerAsnLysGluGlnThrLysLeuTyIleGlnLeuSerGlyArgValThrValSer 220  
QY 690 ACAAAGAGTCAACAAAGCATAGTCCCTTAATATCGATCGATAGCGTGGTGGTGGGT 749  
Db 221 ThrLysArgSerGlnGlnThrIleProAsnIleGlySerArgProArgValArgGly 240  
QY 750 CAATCAGGAGGATAGCATATATCTGACCATTTGTAAACCTGGAGATATCTTAATGATA 809  
Db 241 GlnSerGlyArgIleSerIleTyTrpThrIleValLysProGlyAspIleLeuMetIle 260  
QY 810 AACAGTAATGGCAACTTAGTTGACCGCGGGGATTTTAAATGAAAACAGGGAAGC 869  
Db 261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyPheLysLeuLysThrGlyLysSer 280  
QY 870 TCTGTATAGATCAGATGACCATCAGATTTGTGTCTGAATGTATTACACCAAT 929  
Db 281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn 300  
QY 930 GGAAGCATCCCAACGACAAACCATTTTCAAAATGTGAAACAAAGTTACATATATGAAATGC 989

Db 301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyGlyLysCys 320  
QY 990 CCCAAGTATATCAGCAAAACACATTAAAGCTGGCCACTGGATGAGCAATATACAGAA 1049  
Db 321 ProLysTyTrpIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu 340  
QY 1050 AAGCAAAATCAGA 1061  
Db 341 LysGlnIleArg 344

RESULT 9  
US-09-232-468A-22  
; Sequence 22, Application US/09232468A  
; Patent No. 6207165  
; GENERAL INFORMATION:  
; APPLICANT: AUDONNET et al.  
; TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE FORMULA AGAINST PORCINE  
; TITLE OF INVENTION: REPRODUCTIVE AND RESPIRATORY PATHOLOGIES  
; FILE REFERENCE: 454313-2230  
; CURRENT APPLICATION NUMBER: US/09/232,468A  
; CURRENT FILING DATE: 1999-01-05  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 566  
; TYPE: PRT  
; ORGANISM: swine influenza virus  
; US-09-232-468A-22

Alignment Scores:  
Pred. No.: 7,55e-142 Length: 566  
Score: 1427.50 Matches: 262  
Percent Similarity: 85.51% Conservative: 33  
Best Local Similarity: 75.94% Mismatches: 49  
Query Match: 74.66% Indels: 1  
DB: 3 Gaps: 1

US-10-826-929A-1 (1-1061) x US-09-232-468A-22 (1-566)

QY 30 ATGAGACACACCATTTTGTACTACTACCTGAGCCCTTGTCTACAGTCAAAAC---CCA 86  
Db 1 MetLysThrValIleAlaLeuSerTyIlePheCysLeuValLeuGlyGlnAspLeuPro 20  
QY 87 ACCAGTGAACAAACACACAGCCACATTTATGCTGGGACACCATGCTAGTACCAATGGAACA 146  
Db 21 GluAsnGlySerSerThrAlaLysProGlyLeuGlyHisHisAlaValProAsnGlyThr 40  
QY 147 TTGGTAAACAAATACATGATGACCAAAATGAGGTGACAAATGCTACTGAAATAGTTCAG 206  
Db 41 LeuValLysThrIleThrAsnAspGlnIleGluValThrAsnAlaThrGluLeuValGln 60  
QY 207 ACATTTCAATAGGGAATATGCAACAACTCATATAAGTTCTAGATGGAAGAAATTCG 266  
Db 61 SerPheSerMetGlyLysIleCysAsnAsnProHisArgValLeuAspGlyAlaAsnCys 80  
QY 267 ACATTAATAGATGCAATGCTAGGACACCCCACTGCTGTGATGCTTCCAGTATGAGAAATTCG 326  
Db 81 ThrLeuIleAspAlaLeuLeuGlyAspProHisCysAspGlyPheGlnAsnGluLysTrp 100  
QY 327 GACCTCTTCATAGAAAGAGAGCGCTTTCAGCAATGCTACCAATGCTACCATATCACCTCCG 386  
Db 101 AspLeuPheValGluArgSerLysCysPheSerAsnCysTyProTyArgValProAsp 120  
QY 387 TATGATCCCTCGGTCCATTGTAGCATCTCAGGAACATTAAGAATTCACAGCAGAGGGA 446  
Db 121 TyrAlaSerLeuArgSerLeuIleAlaSerSerGlyThrLeuGluPheIleAsnGluGly 140  
QY 447 TTCATATGACAGAGGTGCTACTCAAAACGGAAGAGTGGAGCTTCGCAAAAGGGGATCAGCC 506  
Db 141 PheAsnTrpThrGlyValThrGlnAsnGlyGlySerAsnAlaCysLysArgGlyProAsp 160  
QY 507 GATAGTTCTTTAGCCGACTGAATGGCTATACAAATCTGGAACACTCTTACCCCATTCG 566

Db 261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLeuLeuLysThrGlyLysSer 280  
QY 870 TCTGTAAATCAGATCAGATCCACCCATAGACATTTGCTGCTGAATGATTACACCAAT 929  
Db 281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn 300  
QY 930 GGAAGCATCCCCAGACAAACCAATTTCAAAATGTGAACAAAGTTACATATGGAATAATGC 989  
Db 301 GlySerIleProAsnAspLysProPheGlnValAsnLysValThrGlyLysCys 320  
QY 990 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1049  
Db 321 ProLysTyrIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu 340  
QY 1050 AAGCAAAATCAGA 1061  
Db 341 LysGlnIleArg 344

## RESULT 7

US-10-065-133A-8.  
; Sequence 8, Application US/10065133A  
; Patent No. 6685946  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/065,133A  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 8  
; TYPE: PRT  
; ORGANISM: Equine influenza virus H3N8  
US-10-065-133A-8

## Alignment Scores:

Pred. No.: 8,756-180 Length: 565  
Score: 1787.00 Matches: 333  
Percent Similarity: 99.42% Conservative: 9  
Best Local Similarity: 96.80% Mismatches: 2  
Query Match: 93.46% Indels: 0  
DB: 4 Gaps: 0

US-10-826-929A-1 (1-1061) x US-10-065-133A-8 (1-565)

QY 30 ATGAGACAAACCAATTTATTTGATCTACTGACCCATTTGGTCTACAGTCAAAACCAACC 89  
Db 1 MetLysThrIleLeuLeuIleProLeuThrHisTrpValTyrSerGlnAsnProThr 20  
QY 90 AGTGGAAACAACAGACCAATTTATGCTGGGACACCACTGACAGTACGAAATGCAATG 149  
Db 21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40  
QY 150 GTAAACAAATCACTGATGACCAAAATGTAGGTGACAAATGCTACTGAAATGCTCAGAC 209  
Db 41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60  
QY 210 ATTTCAATAGGGAATATGCAACAACTCATATTAAGTTCTAGATGGAATGCA 269  
Db 61 IleSerIleGlyLeuIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr 80  
QY 270 TTAATAGATGCAATGCTAGGACACCCCACTGCTGTCTTCAGTATGAGAAATGGGAC 329  
Db 81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyrGluAsnTrpAsp 100  
QY 330 CTCCTTCATAGAAGACGACGCTTTACGAAATGCTACCCATATGACATCCCTGACTAT 389

Db 101 LeuPheIleGluArgSerSerAlaPheSerSerCysTyrProTyrAspIleProAspTyr 120  
QY 330 GCATCGCTCCGCTCCATTTGATAGCATCTCCTCAGAAATAGATTCACACAGCAGAGGATTC 449  
Db 121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140  
QY 450 ACATGGACAGGTGTCACTCAAAACGGAAGAGTGGAGCTCGCAAAAGGGGATCAGCCGAT 509  
Db 141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlySerCysLysArgGlySerAlaAsp 160  
QY 510 AGTTCTTTTCCGACGACTAATTTGGTAAACAAATCTGAAAACCTTTACCCACATGAAAT 569  
Db 161 SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyrProThrLeuAsn 180  
QY 570 GTGCAATGCTCTAACAATAAAATTTCCGACAAACCTATACATCTGGGGGATTCATCACCG 629  
Db 191 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleTrpGlyIleHisHisPro 200  
QY 630 AGCTCAAAACCAACAGCAGACAGAAATTTGATACATCCAAAGATCAGGACGAGTAACTCTCA 689  
Db 201 SerSerAsnLysGluGlnThrThrLysLeuTyrIleGlnGluSerGlyArgValThrValSer 220  
QY 690 ACAAAGAAAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGTGGTGGGT 749  
Db 221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProArgValArgGly 240  
QY 750 CAATCAGGACGAGTAAGCATATATCTGGACCATTTGAAACCTGGAGATATCTTAATGATA 809  
Db 241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle 260  
QY 810 AACAGTAAATGCACTAGTTGTCACCGCGGGGATATTTAAATTTGAAACAGGGAAGAC 869  
Db 261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuLysThrGlyLysSer 280  
QY 870 TCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 929  
Db 281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn 300  
QY 930 GGAAGCATCCCCAGACAAACCAATTTCAAAATGTGAACAAAGTTACATATGGAATAATGC 989  
Db 301 GlySerIleProAsnAspLysProPheGlnValAsnLysValThrTyrGlyLysCys 320  
QY 990 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1049  
Db 321 ProLysTyrIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu 340  
QY 1050 AAGCAAAATCAGA 1061  
Db 341 LysGlnIleArg 344

## RESULT 8

US-10-434-811A-8  
; Sequence 8, Application US/10434811A  
; Patent No. 6824784  
; GENERAL INFORMATION:  
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher  
; APPLICANT: Education  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C1-PUS-1  
; CURRENT APPLICATION NUMBER: US/10/434,811A  
; CURRENT FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 8  
; LENGTH: 565  
; TYPE: PRT  
; ORGANISM: Equine influenza virus H3N8

```
QY 270 TTAATAGATCAATGCTAGGAGACCCCACTGTGATGCTTCCAGTATGAGAAATGGGAC 329
Db 81 LeuileaspAlaMetLeuGlyArgProHisCysaspValPheGlnTyrGluasnTrpAsp 100
QY 330 CTCTTCATAGAAAGACGACGGCTTTCAGCAATGTCTACCAATATGACATACCTGACTAT 389
Db 101 LeuPheileGluArgSerSerAlaPheSerCysTyrProTyrAspIleProAspTyr 120
QY 390 GCATCGCTCCGGTCCATGTAGCATCTCAGGAACATTAGAATTCACAGCAGGAGATTC 449
Db 121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140
QY 450 ACATGGACAGGTGTCTCACTCAAAACGGAAGTGGAGCTCGCAAAAGGGGATCAGCCGAT 509
Db 141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlySerCysIysArgGlySerAlaAsp 160
QY 510 AGTTCTTTAGCGACTGAATTCGCTAACCAAAATCTGGAACCTTCAACCCCACTGATTC 569
Db 161 SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyrProThrLeuAsn 180
QY 570 GTGACAAATGCTAGCAATTCGCTAACCAAAATCTGGAACCTTCAACCCCACTGATTC 629
Db 201 SerSerAsnLysGluGlnThrLysLeuTyrIleGlnGluSerGlyArgValThrValSer 220
QY 630 AdCTCAAAACCAACAGCAGACAGCAATTCATCACTCAAGAAATCTGGAACCTTCAACCCCACTGATTC 689
Db 201 SerSerAsnLysGluGlnThrLysLeuTyrIleGlnGluSerGlyArgValThrValSer 220
QY 690 AAAAAAGAGTCAACAAAGATAGTCCCTTAATATCGATTCAGATCGGAGTTCAGGATTC 749
Db 221 ThrLysArgSerGlnGlnThrIleProAsnIleGlySerArgProArgValArgGly 240
QY 750 CNAATGAGGAGGATAGCATATATGAGCACTGATTAACCTGAGATATCTTAATGATA 809
Db 241 GlnSerGlyArgIleSerIleTyrTrpThrIleValProGlyAspIleLeuMetIle 260
QY 810 AACAGTAATGGCAACTTAGTTCACCGCGGGATATTTAAATTTGAAAAACAGGAAAAAGC 869
Db 261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuLysThrGlyLysSer 280
QY 870 TCTGTAATGAGATCAGATGACCCATAGACATTTGCTGTGTCTGTAATGATTCACCAAT 929
Db 281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn 300
QY 930 GGAAGCATCCCAACGACAAACACTTTAAAGCTGGCACTGGGATGAGGAATATACCAAGAA 1049
Db 301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 320
QY 990 CCAAGTATATCAGGCAAAACACTTTAAAGCTGGCACTGGGATGAGGAATATACCAAGAA 1049
Db 321 ProLysTyrIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu 340
QY 1050 AGCAAAATCAGA 1061
Db 341 LysGlnIleArg 344
```

## RESULT 6

```
US-09-762-861B-8
; Sequence 8, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-CI-PUS (formerly HKZ-033CPUS)
; CURRENT APPLICATION NUMBER: US/09/762,861B
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
```

```
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-09-762-861B-8
```

```
Alignment Scores:
Pred. No.: 8,75e-180 Length: 565
Score: 1787.00 Matches: 333
Percent Similarity: 99.42% Conservative: 9
Best Local Similarity: 96.80% Mismatches: 2
Query Match: 93.46% Indels: 0
DB: 4 Gaps: 0
```

US-10-826-929A-1 (1-1061) x US-09-762-861B-8 (1-565)

```
QY 30 ATGAAGACAAACCATTTATTTTGTATCTACTGACCCATTTGGTCTTACAGTCAAAACCCCAACC 89
Db 1 MetLysThrThrIleIleLeuIleProLeuThrHisTrpValTyrSerGlnAsnProThr 20
QY 90 AGTGGAAACAAACACAGCCACATTTATGTCTGGGACACCATCGCAGTAGCAAAATCGAAACATTG 149
Db 21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40
QY 150 GTAAAAACAATCACTGATGATCCAAATTTGAGGTGACAAATGCTCAATAGTTCAGAGC 209
Db 41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60
QY 210 ATTTCAATAGGAAAAATATGCAACAACTCATATAAGTTCTAGATGGAAGAAATTCACACA 269
Db 61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr 80
QY 270 TTAATAGATCAATGCTAGGAGACCCCACTGTGATGCTTCCAGTATGAGAAATGGGAC 329
Db 81 LeuileaspAlaMetLeuGlyArgProHisCysaspValPheGlnTyrGluasnTrpAsp 100
QY 330 CTCTTCATAGAAAGACGACGGCTTTCAGCAATGTCTACCAATATGACATACCTGACTAT 389
Db 101 LeuPheileGluArgSerSerAlaPheSerCysTyrProTyrAspIleProAspTyr 120
QY 390 GCATCGCTCCGGTCCATGTAGCATCTCAGGAACATTAGAATTCACAGCAGGAGATTC 449
Db 121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140
QY 450 ACATGGACAGGTGTCTCACTCAAAACGGAAGTGGAGCTCGCAAAAGGGGATCAGCCGAT 509
Db 141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlySerCysIysArgGlySerAlaAsp 160
QY 510 AGTTCTTTAGCGACTGAATTCGCTAACCAAAATCTGGAACCTTCAACCCCACTGATTC 569
Db 161 SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyrProThrLeuAsn 180
QY 570 GTGACAAATGCTAGCAATTCGCTAACCAAAATCTGGAACCTTCAACCCCACTGATTC 629
Db 181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleTrpGlyIleHisHisPro 200
QY 630 AGCTCAAAACCAACAGCAGACAGCAATTTGATCCAAAGATCAGGACGAGTAACAGTCTCA 689
Db 201 SerSerAsnLysGluGlnThrLysLeuTyrIleGlnGluSerGlyArgValThrValSer 220
QY 690 AAAAAAGAGTCAACAAAGATAGTCCCTTAATATCGATTCAGATCGGAGTTCAGGATTC 749
Db 221 ThrLysArgSerGlnGlnThrIleProAsnIleGlySerArgProArgValArgGly 240
QY 750 CAATCAGCAGGATAGCATATATGAGCACTGATTAACCTGAGATATCTTAATGATA 809
Db 241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle 260
QY 810 AACAGTAATGGCAACTTAGTTCACCGCGGGATATTTAAATTTGAAAAACAGGAAAAAGC 869
```



Db	201	SerSerAsnLysGluGlnThrLysLeuTyrIleGlnGluSerGlyArgValThrValSer	220
Qy	690	ACAAAAAGAGAGTCAACAAACGATAGTCCCTAAATATCGGATCTAGACCGTGGGTAGGGGT	749
Db	221	ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProIrpValArgGly	240
Qy	750	CAATCAGCGAGGATAAGCAVATATCTGCACCAATCTGAAACCTGGAGATATCCCTAAATGATA	809
Db	241	GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuThrIle	260
Qy	810	AACAGTAAATGGCAACTTAGTTGCACCGGGGATATTTTAAATGAAAAACAGGAAAAAGC	869
Db	261	AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuLysThrGlyLysSer	280
Qy	870	TCGTGTAATGAGATCAGATGCACCATAGACATTTGTGTGTGTCGTAAGTATATTACACCAAT	929
Db	281	SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn	300
Qy	930	GDAAGCATCCCCAACGACAAACCAATTTCAAANGTGAAACAGTTACATATGGAATGC	989
Db	301	GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys	320
Qy	990	CCCAAGTATATCAGGCAAAAAACATTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA	1049
Db	321	ProLysTyrIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu	340
Qy	1050	ANGCAATCAGA	1061
Db	341	LysGlnIleArg	344

### RESULT 3

US-10-065-133A-11  
; Sequence 11, Application US/10065133A

; Patent No. 5665946  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DOWLING, Patricia W.  
 ; APPLICANT: Youngner, Julius S.  
 ; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES

FILE REFERENCE: EQ-1-C2-1  
CURRENT APPLICATION NUMBER: US/10/065,133A

; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: PCT/US99/185583

; PRIORITY NUMBER: 101/0000/1  
 ; PRIORITY FILING DATE: 1999-08-12  
 ; PRIORITY APPLICATION NUMBER: 09/133-921

; PRIORITY APPLICATION NUMBER: 108  
 ; PRIOR FILING DATE: 1998-01-10  
 ; NUMBER OF SEQ IN NOS: 108

; NUMBER OF D  
; SOFTWARE: P  
; SEQ TO NO 11

```

; SEQ ID NO 11
; LENGTH: 565
; TYPE: CDS

```

Alignment Scored:		
Pred. No.:	1.6e-180	565
Score:	1794.00	333
Percent Similarity:	99.43%	Conservative: 2
Best Local Similarity:	96.80%	Mismatches: 2
Query Match:	93.83%	Indels: 0
DB:	4	Gaps: 0

US-10-826-929A-1 (1-1061) x US-10-065-133A-11 (1-565)

Qy	30	ATGAGACAAACCATTTATTTGATACTACTGACCCATTTGGGTCTACAGTCAAAACCCCAACC	89
Db	1	MetLysThrThrIleLeuLeuLeuLeuThrHisItrpValTyrSerGlnAsnProThr	20
Qy	90	AGTGGAAACAACACAGCCACATTTATGCTGGGACACCATCGAGTAGCAAAATGGAACATTG	149
Db	21	SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu	40
Qy	150	GTAATAACAATAACTGATGACCAAAATTCAGGTGACAAATGCTACTGTAATTTAGTTTCAGAGC	209



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model  
Run on: February 27, 2005, 18:16:22 ; Search time 40 Seconds  
(without alignments)  
3960.133 Million cell updates/sec

Title: US-10-826-929A-1  
Perfect score: 1912  
Sequence: 1 agcaaaagcgggatattt.....taccagaaaagcaaatcaga 1061

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DRV=xlpl  
-Q=/cgn2\_1/USPTO.spool\_P/US10826929/runat\_27022005\_095244\_27608/app\_query.fasta\_1.1223  
-DB=Issued Patents AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTPWT=ptp -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10826929 -@CGN\_1\_46 -runat\_27022005\_095244\_27608 -NCPUL=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEVTIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1794	93.8	565	4	US-09-506-286B-11
2	1794	93.8	565	4	US-09-762-861B-11
3	1794	93.8	565	4	US-10-065-133A-11
4	1794	93.8	565	4	US-10-434-811A-11
5	1787	93.5	565	4	US-09-506-286B-8
6	1787	93.5	565	4	US-09-762-861B-8
7	1787	93.5	565	4	US-10-065-133A-8
8	1787	93.5	565	4	US-10-434-811A-8
9	1427.5	74.7	566	3	US-09-232-468A-22
10	1427.5	74.7	566	4	US-09-784-984B-53
11	1421	74.3	570	2	US-08-453-848-7
12	1421	74.3	570	3	US-09-169-027-7

13	1404.5	73.5	571	2	US-08-453-848-15	Sequence 15, Appl
14	1404.5	73.5	571	3	US-09-169-027-15	Sequence 15, Appl
15	1398.5	73.1	571	2	US-08-453-848-21	Sequence 21, Appl
16	1398.5	73.1	571	3	US-09-169-027-21	Sequence 21, Appl
17	1373	71.8	347	3	US-09-217-293-1	Sequence 1, Appl
18	624.5	32.7	569	3	US-08-686-968C-227	Sequence 227, App
19	588	30.8	566	4	US-09-232-468A-14	Sequence 14, Appl
20	588	30.8	566	4	US-09-784-984B-51	Sequence 51, Appl
21	580	30.3	572	2	US-08-453-848-9	Sequence 9, Appl
22	580	30.3	572	3	US-09-169-027-9	Sequence 9, Appl
23	393	20.6	347	1	US-08-229-781-58	Sequence 58, Appl
24	393	20.6	347	1	US-08-630-918-58	Sequence 58, Appl
25	393	20.6	347	3	US-09-004-422-58	Sequence 58, Appl
26	393	20.6	347	4	US-09-918-568-58	Sequence 58, Appl
27	321.5	16.8	165	1	US-08-120-607A-7	Sequence 7, Appl
28	215.5	11.3	585	2	US-08-453-848-11	Sequence 11, Appl
29	215.5	11.3	585	3	US-09-169-027-11	Sequence 11, Appl
30	209.5	11.0	589	2	US-08-453-848-13	Sequence 13, Appl
31	209.5	11.0	589	3	US-09-169-027-13	Sequence 13, Appl
32	209	10.9	592	2	US-08-453-848-17	Sequence 17, Appl
33	209	10.9	592	3	US-09-169-027-17	Sequence 17, Appl
34	207.5	10.9	345	1	US-07-954-840A-18	Sequence 18, Appl
35	206.5	10.8	345	1	US-07-954-840A-12	Sequence 12, Appl
36	204	10.7	586	2	US-08-453-848-19	Sequence 19, Appl
37	204	10.7	586	3	US-09-169-027-19	Sequence 19, Appl
38	201.5	10.5	345	1	US-07-954-840A-10	Sequence 10, Appl
39	200.5	10.5	345	1	US-07-954-840A-14	Sequence 14, Appl
40	200.5	10.5	345	1	US-07-954-840A-24	Sequence 24, Appl
41	199.5	10.4	345	1	US-07-954-840A-8	Sequence 8, Appl
42	198.5	10.4	345	1	US-07-954-840A-16	Sequence 16, Appl
43	198.5	10.4	345	1	US-07-954-840A-31	Sequence 31, Appl
44	195.5	10.2	345	1	US-07-954-840A-26	Sequence 26, Appl
45	194.5	10.2	345	1	US-07-954-840A-20	Sequence 20, Appl

#### ALIGNMENTS

RESULT 1  
US-09-506-286B-11  
; Sequence 11, Application US/09506286B  
; Patent No. 6482414  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; APPLICANT: The University of Pittsburgh, of the Commonwealth  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2  
; CURRENT APPLICATION NUMBER: US/09/506,286B  
; CURRENT FILING DATE: 2000-02-16  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 565  
; TYPE: PRT  
; ORGANISM: Equine influenza virus H3N8  
US-09-506-286B-11

Alignment Scores:  
Pred. No.: 1 6e-180 Length: 565  
Score: 1794.00 Matches: 333  
Percent Similarity: 99.42% Conservatives: 9  
Best Local Similarity: 96.80% Mismatches: 2  
Query Match: 93.83% Indels: 0  
DB: 4 Gaps: 0

US-10-826-929A-1 (1-1061) x US-09-506-286B-11 (1-565)

QY 30 ATGAAGACCAACCATTTATTTGATCTACTGACCCATTGGTCTACGTAAACCAACC 89  
|||||

**This Page Blank (uspto)**

```

XX DT 28-OCT-1998 (first entry)
XX DE SIV strain H3N2 haemagglutinin.
XX KW Multivalent vaccine; pig; pathogen; respiratory disease; SIV; PRRSV;
XX KW HCV; digestive disease; Aujeszky's disease virus; pseudorabies virus;
XX KW vaccine; swine herpesvirus 1; swine influenza virus; hog cholera virus;
XX KW vector; porcine respiratory and reproductive syndrome virus;
XX KW haemagglutinin; SIRS; swine infertility and respiratory syndrome virus;
XX KW Actinobacillus pleuropneumoniae.
XX OS Swine influenza virus.
XX PN PR2751224-A1.
XX PD 23-JAN-1998.
XX PF 19-JUL-1996; 96FR-00009338.
XX PR 19-JUL-1996; 96FR-00009338.
XX PA (INMR ) RHONE MERIEUX SA.
XX PP WPI; 1998-112824/11.
XX DR N-PSDB; AAV49298.
XX PT Multi-valent polynucleotide vaccines for pigs - consist of at least 3
XX PT plasmids able to express protective antigens from specified viruses.
XX PS Example 12; Fig 10; 63pp; French.
XX CC The invention relates to a multivalent vaccine for protecting pigs
XX CC against several pathogens, especially pathogens associated with
XX CC respiratory and digestive diseases. The pathogens are especially selected
XX CC from Aujeszky's disease virus, swine influenza virus (SIV), porcine
XX CC respiratory and reproductive syndrome virus (PRRSV), hog cholera virus
XX CC (HCV) and Actinobacillus pleuropneumoniae. The vaccines are preferably
XX CC composed of polynucleotide sequences encoding 3 antigens, all as part of
XX CC vectors. This sequence represents the SIV strain H3N2 haemagglutinin
XX CC protein. The coding sequence was subcloned into the plasmid pVR1012 to
XX CC generate plasmid pPB144 for use in the vaccine
XX SQ Sequence 566 AA;
XX
Alignment Scores:
Pred. No.: 4.48e-134 Length: 566
Score: 1427.50 Matches: 262
Percent Similarity: 85.51% Conservative: 33
Best Local Similarity: 75.94% Mismatches: 49
Query Match: 74.66% Indels: 1
DB: Gaps: 2
US-10-826-929A-1 (1-1061) x AAW68406 (1-566)
QY 30 ATGAAGACACCAATATTGTTGATCTACTGACCCATTGGTGGTCTACAGTCAAAAC---CCA 86
Db 1 McLeYthrValIleAlaLeuSerTyrllePheCysLeuValleuGlyGlnAspLeuPro 20
QY 87 ACCAGTGGAAACACACAGCCACCATTTATGTCGGGACACCATCGAGTAGCAATGGAACA 146
Db 21 GluAsnGlySerSerThrAlaLysProGlyLeuGlyHisHisAlaValProAsnGlyThr 40
QY 147 TTGGTAAACAAATACATGATGACCAAAATGAGGTGACAAATGCTACTGAATAGTTTCAG 206
Db 41 LeuValLysThrIleThrAsnAspGlnIleGluValThrAsnAlaThrGluLeuValGln 60
QY 207 AGCATTTCAATAGGGAAATATGCACAACTCATATAAGTTCTAGATCGAAGAATTCG 266
Db 61 SerPheSerWetGlyLysIleCysAsnAsnProHisArgValLeuAspGlyAlaAsnCys 80
QY 267 ACATTAATAGATGCAATGCTAGGAGACCCCACTGTGATGTCCTCCAGTATGAGAATTGG 326

```

```

Db 81 ThrLeuIleAspAlaLeuLeuGlyAspProHisCysAspGlyPheGlnAsnGluLysTrp 100
QY 327 GACCTCTTCATAGAAAGAGAGAGCGCTTTTCAGCAATTTGCTACCCATATGATCATCCCTGAC 386
Db 101 AspLeuPheValGluArgSerLysCysPheSerAsnCysTyPProTyRaspValProAsp 120
QY 387 TATGATCCCTCCGGTCCATCTTAGCATCTCTCAGGAACATTAGAATTTTCAGCAGAGGGA 446
Db 121 TyrAlaSerLeuArgSerLeuIleAlaSerSerGlyThrLeuGluPheIleAsnGluGly 140
QY 447 TTCACATGGACAGGTGTCTACTCAAAACGGAAGAGTGGAGCTGCCAAAAGGGGATCAGCC 506
Db 141 PheAsnTrpThrGlyValThrGlnAsnGlyGlySerAsnAlaCysLysArgGlyProAsp 160
QY 507 GATAGTTTCTTTAGCCGACTGAATGGCTAAACAAATCTGGAACACTTACCCCATTTG 566
Db 161 SerGlyPhePheSerArgLeuAsnTrpLeuTyLysSerGlyAsnThrTyRProMetLeu 180
QY 567 AATGTGACAAATGCTTAAACAATAAAATTTTCGACAAACTATACATCTGGGGGATTCATCAC 626
Db 181 AsnValThrMetProAsnSerAspAsnPheAspLysLeuTyrlleTrpGlyValHisHis 200
QY 627 CCGAGCTCAACAAACAGCAGACAGAAATTTGTATCATCCAAAGATCAGGACGAGTAACAGTC 686
Db 201 ProSerThrAspArgGluGlnThrAsnLeuTyRValGlnValSerGlyLysAlaThrVal 220
QY 687 TCAACAAAAGAGTCAACAAACGATAGTCCCTTAATATCGGATCTAGACCGTGGTTAGG 746
Db 221 PheThrLysArgSerGlnGlnThrIleIleProAsnSerArgSerArgProTrpValArg 240
QY 747 GGTCAATCAGGAGGATAGCATATACTGGACCATTTGTAACACCTTGAAGATATCCTAATG 806
Db 241 GlyLeuSerSerArgIleSerIleHisTrpThrIleValLysProGlyAspIleLeuIle 260
QY 807 ATAAACAGTAATGGCAACTTAGTTCACCGCGGGGATATTTTAAATTTGAAAACAGGAAA 866
Db 261 IleAsnSerAsnGlyAsnLeuIleAlaProArgGlyTyRPhelLysMethHisAsnGlyArg 280
QY 867 AGCTCTGTAATGAGATCAGATCCACCCATAGACATTTGTGTCTGTAATGTATTACACCA 926
Db 281 SerSerIleMetArgSerAspAlaProIleGlyThrCysSerSerGluCysIleThrPro 300
QY 927 AATGGAAGCATCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTTACATATGAAAA 986
Db 301 AsnGlySerIleProAsnAspLysProPheGlnAsnValAsnLysIleThrTyRglyAla 320
QY 987 TGCCCCAAAGTATATCAGGCAAAACACTTTTAAAGCTGGCCACTGGGATGAGGAATATACCA 1046
Db 321 CysProLysTyRValLysGlnAsnThrLeuLysLeuAlaThrGlyWetArgAsnIlePro 340
QY 1047 GAAAAGCAAAATCAGA 1061
Db 341 GluLysGlnThrArg 345

```

Search completed: February 27, 2005, 18:24:54

Job time : 198 secs



QY 795 GATATCTTAATGATAACACATTAATGCAACTTGTGCTGACCGCGGATATTTAAATG 854  
 Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 260  
 QY 855 AAAACAGGGAAGCTCTGTAATGAGATGACATGACACCCATAGACATTTGTGTCTGAA 914  
 Db ::|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 280  
 QY 915 TGATTATACCAATGGAAGCATCCCAACGACGACAAACCATTTCAAATGTGAACAAGTT 974  
 Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 300  
 QY 975 ACATATGGAAGTCCCCAGTATATACAGCAAAACACTTTAAAGCTGGCCACTGGGATG 1034  
 Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 320  
 QY 1035 AGGAATATACCAAGAAAGCAAAATCAGA 1061  
 Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 329

## RESULT 13

ID ABP53897  
 XX ABP53897 standard; protein; 329 AA.

AC ABP53897;

XX 07-JAN-2003 (first entry)

DE Influenza A virus (A/Bangkok/(H3N2)) haemagglutinin partial protein.

KW Influenza; Influenza A virus; pathogenicity; RNA viral disease;

KW viral infection; selenium; vaccine; virucide; anti-HIV.

OS Influenza A virus.

PN WO200278717-A2.

PD 10-OCT-2002.

XX 26-MAR-2002; 2002WO-EP003025.

XX 28-MAR-2001; 2001US-00819387.

XX (NEST ) SOC PROD NESTLE SA.

PA (UNIC-) UNIV NORTH CAROLINA.

XX Beck M, German B, Levander O, Van Dael P;

XX WPI; 2002-759948/82.

DR N-PSDB; ABQ82726.

PT Treatment of influenza or reducing the risk of contracting influenza  
 involves administering selenium to an individual.

PS Example 1; Page; 31pp; English.

CC The present invention describes a method for treating influenza or  
 CC reducing the risk of contracting influenza, which involves administering  
 CC selenium to an individual. Also described is a method for enhancing the  
 CC efficacy of a viral vaccine by administering an antioxidant, preferably  
 CC selenium, to an individual receiving the viral vaccine. The method can be  
 CC used for treating influenza, for reducing the risk of contracting  
 CC influenza, and for enhancing the efficacy of viral vaccine (preferably  
 CC influenza vaccine) in an infant, elderly, a patient or a pet. It can also  
 CC be used for treating virus such as coxsackie and HIV virus. The method  
 CC provides an improved treatment for viral infection, by reducing in vivo  
 CC mutations of the RNA virus. The method also improves a vaccine used to  
 CC prevent transmission of an RNA viral disease. The present sequence  
 CC represents the haemagglutinin protein from Influenza A virus  
 CC (A/Bangkok/(H3N2)). N.B. The present sequence is not given in the  
 CC specification, but is taken from the Genbank accession number AF008899,  
 CC as specified on page 7

XX SQ Sequence 329 AA;  
 Alignment Scores:  
 Pred. No.: 1,31e-135 Length: 329  
 Score: 1442.00 Matches: 258  
 Percent Similarity: 89.57% Conservative: 34  
 Best Local Similarity: 79.14% Mismatches: 34  
 Query Match: 75.42% Indels: 0  
 DB: 5 Gaps: 0  
 US-10-826-929A-1 (1-1061) x ABP53897 (1-329)  
 QY 84 CCAACACAGTGGAAACAAACACGACCATATGCTCTGGACACCATGACGTAGCAATGGA 143  
 Db 4 ProGlyAsnAspAsnSerThrAlaThrLeuCyLeuGlyHisAlaValProAsnGly 23  
 QY 144 ACATTTGGTAAAAACAATAACTGATGACCAAAATGAGGTGACAAATGCTACTGATTTAGTT 203  
 Db 24 ThrLeuValysThrIleThrAsnAspGlnIleGluValThrAsnAlaThrGluLeuVal 43  
 QY 204 CAGAGCATTTCAATAGCGGAAATATGCAACACTCATATAAGTTCTAGATGGAAGAAT 263  
 Db 44 GlnSerSerSerThrGlyArgIleCysAspSerProHisArgIleLeuAspGlyLysAsn 63  
 QY 264 TGCACATTAATAGATGCAATGCTAGGAGACCCCACTGTGATGCTCTCCAGTATGAGAAT 323  
 Db 64 CysThrLeuIleAspAlaLeuLeuGlyAspProHisCysAspGlyPheGlnAsnGluLys 83  
 QY 324 TGGGACCTCTTCATAGAAAGAGCAGCGCTTTTCAGCAATTTGCTACCATATGACATCCCT 383  
 Db 84 TrpAspLeuPheValGluArgSerLysAlaPheSerAsnCysTyrProTyrAspValPro 103  
 QY 384 GACTATGCTATGCTCCGTCCTAGTGTAGCATCTCTAGGAACATTAGAAATTCACAGCAGAG 443  
 Db 104 AspTyrAlaSerLeuArgSerLeuValAlaSerSerGlyThrLeuGluPheIleAsnGlu 123  
 QY 444 GGATTCACATGGACAGCTGTCTCAAAACGGAAGAGTGGAGCGCTGCAAAAGGGGATCA 503  
 Db 124 GlyPheAsnTrpThrGlyValThrGlnSerGlyGlySerTyrAlaCysLysArgGlySer 143  
 QY 504 GCCGATAGTTCTTTAGCCGACTGAATTCGCTAACAAAAATCTGGAACCTTTTACCCACCA 563  
 Db 144 ValAsnSerPhePheSerArgLeuAsnTrpLeuTyrLysSerGluTyrLysTyrProAla 163  
 QY 564 TTGAATGTGACATGCTAAACAATAAAATTTGCAACAACTATACATCTGGGGGATTCAT 623  
 Db 164 LeuAsnValThrMetProAsnAsnGlyLysPheAspLysLeuTyrIleTrpGlyValHis 183  
 QY 624 CACCCGAGCTCAAAACCAACAGCAGACAGAAATTTGTACATCCAGAAATCAGACAGTAACA 683  
 Db 184 HisProSerThrGluLysGluGlnThrAsnLeuTyrValArgAlaSerGlyArgValThr 203  
 QY 684 GTCTCAACAAAAAGAGTCAACAAACATAGTCCCTTAATATCGATTCGATCGCGGT 743  
 Db 204 ValSerThrLysArgSerGlnGlnThrValIleProAsnIleGlySerArgProTyrVal 223  
 QY 744 AGGGGTCAATCAGCAGGATAGCATATACTGGACCATTTGTAACCTGGAGATATCCTTA 803  
 Db 224 ArgGlyLeuSerSerArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeu 243  
 QY 804 ATGATAAACAGTAATGGCAACTTAGTTGCACCCCGGGGATATTTAAATTTGAAAAACAGGG 863  
 Db 244 LeuIleAsnSerThrGlyAsnLeuIleAlaProArgGlyTyrPheLysIleArgThrGly 263  
 QY 864 AAAAGTCTGTAAATAGATCAGATGACCCCATAGACATTTGTGTGTGAATGATTATACA 923  
 Db 264 LysSerSerIleMetArgSerAspAlaProIleGlyThrCysSerSerGluCysIleThr 283  
 QY 924 CCNAATGGAGCATCCCCAACGACCAACCATTTCAAATGTGCAACAGTTACATATGGA 983  
 Db 284 ProAsnGlySerIleProAsnAspLysProPheGlnAsnValAsnLysIleThrTrpGly 303

Db 201 HisProSerThrAspLysGluGlnThrAsnLeuValGlnAlaSerGlyLysValThr 220  
 Qy 684 GTCTCAACAAAGAGTCAACAAAGATAGTCCCTAATATCGGATCTAGACCGGGTT 743  
 Db 221 ValSerThrLysArgSerGlnGlnThrIlelleProAsnValGlySerArgProTrpVal 240  
 Qy 744 AGGGTCAATCAGGAGGAGTAAAGCATATCTGACCATTTGTAACACCTGGAGATCTTA 803  
 Db 241 ArgGlyLeuSerSerArgIleSerIleTrpThrIleValLysProGlyAspIleLeu 260  
 Qy 804 ATGATAACAGTAATGGCACTAGTTCGACCGCGGGATATTTAAATTTGAAACACAGG 863  
 Db 261 ValIleAsnSerAsnGlyAsnLeuIleAlaProArgGlyTyPheLysMetArgThrGly 280  
 Qy 864 AAAAGCTCTGTAATCAGATCAGATGACCCATAGACATTTGTGCTCTGAATGTATTACA 923  
 Db 281 LysSerSerIleMetArgSerAspAlaProIleGlyThrCysSerSerGluCysIleThr 300  
 Qy 924 CCAATGGAAGCATCCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACATATGA 983  
 Db 301 ProAsnGlySerIleProAsnAspLysProPheGlnAsnValAsnLysIleThrTyGly 320  
 Qy 984 AAATCCCCCAAGTATATCGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATA 1043  
 Db 321 AlaCysProLysTyValLysGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnVal 340  
 Qy 1044 CCAGAAAGCAATCAGA 1061  
 Db 341 ProGluLysGlnThrArg 346

## RESULT 12

ID ABP53894  
 AC ABP53894;

DT 07-JAN-2003. (first entry)

DE Influenza A/Bangkok/1/79 (H3N2), haemagglutinin protein.

KW Influenza; Influenza A virus; pathogenicity; RNA viral disease;

OS Influenza A virus.

FH Key Location/Qualifiers

FT Misc-difference 1..550

/note= "x is unknown"

PN WO20027817-A2.

PD 10-OCT-2002.

PF 26-MAR-2002; 2002WO-EP003025.

PR 28-MAR-2001; 2001US-00819387.

PA (NEST ) SOC PROD NESTLE SA.

PA (UYNC-) UNIV NORTH CAROLINA.

PI Beck M, German B, Levander O, Van Dael P;

DR WPI; 2002-759948/82.

DR N-PSDB; ABQ82723.

PT Treatment of influenza or reducing the risk of contracting influenza

PT involves administering selenium to an individual.

PS Example 1; Page; 31pp; English.

CC The present invention describes a method for treating influenza or

CC reducing the risk of contracting influenza, which involves administering

CC selenium to an individual. Also described is a method for enhancing the

CC efficacy of a viral vaccine by administering an antioxidant, preferably

CC selenium, to an individual receiving the viral vaccine. The method can be

CC used for treating influenza, for reducing the risk of contracting

CC influenza, and for enhancing the efficacy of viral vaccine (preferably

CC influenza vaccine) in an infant, elderly, a patient or a pet. It can also

CC be used for treating virus such as coxsackie and HIV virus. The method

CC provides an improved treatment for viral infection, by reducing in vivo

CC mutations of the RNA virus. The method also improves a vaccine used to

CC prevent transmission of an RNA viral disease. The present sequence

CC represents the haemagglutinin protein from Influenza A/Bangkok/

CC 1/79 (H3N2). N.B. The present sequence is not given in the specification,

CC but is taken from the Genbank accession number J02092, as specified on

CC page 7

SQ Sequence 550 AA;

## Alignment Scores:

Pred. No.: 2,74e-136 Length: 550  
 Score: 1449.50 Matches: 262  
 Percent Similarity: 90.27% Conservative: 35  
 Best Local Similarity: 79.64% Mismatches: 31  
 Query Match: 75.81% Indels: 1  
 Gaps: 1

US-10-826-929A-1 (1-1061) x ABP53894 (1-550)

Qy 78 CAAACACACACAGTGGAACCAACACAGCCACATTATGCTGGGACACCATCGATG 134

Db 1 GlnAsnLeuProGlyAsnAspAsnSerThrAlaThrLeuCysLeuGlyHisAlaVal 20

Qy 135 GCAATGGAACATCTGGTAAACAAATACTGATGACCAAAATGAGGTGACAAATCTACT 194

Db 21 ProAsnGlyThrLeuValLysThrIleThrAsnAspGlnIleGluValThrAsnAlaThr 40

Qy 195 GAATAGTTCAGACATTTCAATAGGAAATATGCAACACTCATATAAGTTCTAGNT 254

Db 41 GluLeuValGlnSerSerSerThrGlyArgIleCysAspSerProHisArgIleLeuAsp 60

Qy 255 GGAGAAATTCACATTAATAGATGCAATGCTAGGAGACCCCACTGTGATCTCTTCCAG 314

Db 61 GlyLysAsnCysThrLeuIleAspAlaLeuLeuGlyAspProHisCysAspGlyPheGln 80

Qy 315 TATGAGAAATGGACCTCTTCATGAAAGAGAGCGGCTTTCAGCAATGCTACCATAT 374

Db 81 AsnGluLysTrpAspLeuPheValGluArgSerLysAlaPheSerAsnCysTrpProTyr 100

Qy 375 GACATCCCTGATGATCGCTCCGTCCTATTGTAGCATCTCTAGGACATTAGAAATTC 434

Db 101 AspValProAspTyrAlaSerLeuArgSerLeuValAlaSerSerGlyThrLeuGluPhe 120

Qy 435 ACAGCAGAGGATTCACATGACAGGTGCTCACTCAAAACGGAAGAGTGGAGCTGCAAA 494

Db 121 IleAsnGluGlyPheAsnTrpThrGlyValThrGlnSerGlyGlySerThrAlaCysLys 140

Qy 495 AGGGATCAGCCGATAGTTCTTTAGCCGACTGAATTCGCTTAACAAATCTGGAACCTCT 554

Db 141 ArgGlySerAspAsnSerPhePheSerArgLeuAsnTrpLeuTrpGluSerLys 160

Qy 555 TACCCCATTCGATGTCACATGCTGCTAACTAAATAAATTCGACAAACTATACATCTGG 614

Db 161 TyrProValLeuAsnValThrMetProAsnAsnGlyAsnPheAspLysLeuTyrIleTrp 180

Qy 615 GGGATTTCATACCCGAGCTCAAAACACAGACAGAGAAATTTGATACATCAAGAAATCAGA 674

Db 181 GlyValHisHisProSerThrAspLysGluGlnThrAsnLeuTrpValArgAlaSerGly 200

Qy 675 CGAGTAACAGTCTCAACAAAAAGAGTCAACAAACGATAGTCCCTTAATATCGATCTAGA 734

Db 201 ArgValThrValSerThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArg 220

Qy 735 CGTGGGTAGGGTCAATCAGGAGGATAGCATATATCTAGCACTTGTAAACCTGGA 794

Db 221 ProTrpValArgGlyLeuSerSerArgIleSerIleTyrTrpThrIleValLysProGly 240

```
QY 687 TCAACAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGTTAGG 746
DB 221 SerThlyArgSerGlnThrValIleProAsnIleGlySerArgProIrpValArg 240
QY 747 GGTCAATCAGCGCAGGATAGCATATATCTGGACCAATTGTAAACCTGGAGATATCTTAATG 806
DB 241 GlyLeuSerSerArgIleSerIleTyrTrpThrIleValProGlyAspIleLeuLeu 260
QY 807 ATAAACAGTAATGGCAACTAGTGTGACCGCGGGATATTTAAATGAAACAGGAAA 866
DB 261 IleAsnSerAsnGlyAsnLeuIleAlaProArgGlyTyrPheIleValArgThrGlyLys 280
QY 867 AGCTCTGTAATGAGATCAGATGACCCATAGACATTTGTGTCTCAATGTATTACACCA 926
DB 281 SerSerIleMetArgSerAspAlaProIleGlyThrCysSerSerGlyCysIleThrPro 300
QY 927 AATGGAAGCATCCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACATATGGA 986
DB 301 AdnGlySerIleProAsnAspLysProPheGlnAsnValAsnLysIleThrTyrGlyAla 320
QY 987 TGCCCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACCA 1046
DB 321 CysProLysTyrValLysGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValPro 340
QY 1047 GAAAGCAAAATCAGA 1061
DB 341 GluLysGlnThrArg 345
```

## RESULT 11

```
AAP40615
ID AAP40615 standard; protein; 386 AA.
XX AC AAP40615;
XX
DT 24-OCT-2003 (revised)
DT 12-FEB-1992 (first entry)
XX
DE Sequence of the X-47 haemagglutinin (HA) molecule contg. the entire HA1
DE and the amino-terminus of HA2.
XX
KW Vaccine; immunogen; antigen; diagnosis; therapy; influenza; virus.
XX
OS Influenza A virus; (H3N2).
XX
FH Key Location/Qualifiers
FT Protein 17..346
FT Peptide /label= HA1
FT Peptide 69..76
FT Peptide /note= "claimed"
FT Peptide 156..176
FT Peptide /note= "claimed"
FT Peptide 294..319
FT Peptide /note= "claimed"
FT Peptide 294..313
FT Peptide /note= "claimed"
FT Peptide 322..345
FT Peptide /note= "claimed"
FT Peptide 342..351
FT Peptide /note= "claimed"
FT Peptide 346..374
FT Peptide /note= "claimed"
FT Protein 347..386
FT Peptide /label= HA2
FT Peptide 347..374
FT Peptide /note= "claimed"
XX
PN W08400687-A.
XX
XX 01-MAR-1984.
XX
XX 23-AUG-1983; 83WO-US001291.
XX
XX
```

```
PR 23-AUG-1982; 82US-00410455.
PR 29-AUG-1983; 83US-00527401.
XX
PA (SCRI-) SCRIPPS CLINIC & RE.
XX
XX Green N, Alexander S;
XX
XX WPI; 1984-062820/10.
XX
PT Immunogenic peptide(s) contg. 8-40 amino acid residues - useful for
PT prevention and treatment of influenza.
XX
XX Disclosure; Fig 1; 45pp; English.
XX
XX When the peptides of the invention (see FT) are administered, they elicit
XX the prodn. of antibodies to neutralise more than one strain of influenza
XX virus and so they are useful for the prevention, diagnosis and treatment
XX of influenza. (Updated on 24-OCT-2003 to standardise OS field)
XX
XX Sequence 386 AA;
XX
```

## Alignment Scores:

```
Pred. No.: 1.34e-138 Length: 386
Score: 1472.00 Matches: 270
Percent Similarity: 87.57% Conservative: 33
Best Local Similarity: 78.03% Mismatches: 41
Query Match: 76.99% Indels: 2
DB: Gaps: 2
```

US-10-826-929A-1 (1-1061) x AAP40615 (1-386)

```
QY 30 ATGAAGACAACCATTTTGTATCTACTGACCCATTGGTGGTCTACAGTCAAAAC---CCA 86
DB 1 MetLysThrIleIleAlaLeuSerTyrIlePheCysLeuValPheAlaGlnAspLeuPro 20
QY 87 ACCAGTGGAAACAAC---ACAGCCACATTATGTCTGGGACACCATGCTAGTACGAAATGA 143
DB 21 GlyAsnAspAsnAsnSerThrAlaThrLeuCysLeuGlyHisHisAlaValProAsnGly 40
QY 144 ACATTGGTAAAAACAATAACTGACCAAAATGAGGTGACAAATGCTACTGCTACTGATTT 203
DB 41 ThrLeuValLysThrIleThrAsnAspGlnIleGluValThrAsnAlaThrGluLeuVal 60
QY 204 CAGAGCATTTCAATAGGGAATAATATGCAACAATCTATATAAAGTTCTACATGAGAAAT 263
DB 61 GlnSerSerSerThrGlyLysIleCysAsnAsnProHisArgIleLeuAspGlyIleAsn 80
QY 264 TGCACATTAATAGATGCAATGCTAGGAGACCCCACTGTGTGATGTCTTCCAGTATGAGAAT 323
DB 81 CysThrLeuIleAspAlaLeuLeuGlyAspProHisCysAspGlyPheGlnAsnGluLys 100
QY 324 TGGGACCTCTTCATAGAAGAAGCAGCGCTTTTCCAGCAATGTCTACCATATGACATCCCT 383
DB 101 TrpAspLeuPheValGluArgSerLysAlaPheSerAsnCysTyrProTyrAspValPro 120
QY 384 GACTATGCATCGCTCGGTCCATTGTAGCATCTCTCAGGAACATTAGAAATTCACAGCAGAG 443
DB 121 AspTyrAlaSerLeuArgSerLeuValAlaSerSerGlyThrLeuGluPheIleAsnGlu 140
QY 444 GGATTACATGACAGAGGTGTCTACTCAAAACGGAAGAAGTGGAGCCCTGCAAAAGGGGATCA 503
DB 141 GlyPheAsnTrpThrGlyValThrGlnAsnGlyGlySerSerAlaCysLysArgGlyPro 160
QY 504 GCCGATAGTTCTTTAGCCGACTGATGGCTAAACAAATCTGGAACCTCTTACCCACACA 563
DB 161 AspSerGlyPhePheSerArgLeuAsnTrpLeuTyrLysSerGlySerThrTyrProVal 180
QY 564 TTGAATGTGACAAATGCCTAAACAATAAAATTTTCGACAAACTATACATCTGGGGGATTCAT 623
DB 181 GlnAsnValThrMetProAsnAsnAspAsnSerAspLysLeuTyrIleTrpGlyValHis 200
QY 624 CACCCGAGCTCAACCAACAGCAGAGAAATTTGTATCCAAAGATTCAGAGCAGGTAAACA 683
```

Db 144 AspSerGlyPhePheSerArgLeuAsnTrpLeuTyrLysSerGlySerAlaTyrProVal 163  
 QY 564 TTGAATGTGACAAATGCTTAACTAAATTTTCGACAACTATACATCTGGGGATTCTAT 623  
 Db 164 LeuAsnValThrMetProAsnAsnAspAsnPheAspLysLeuTyrIleTrpGlyValHis 183  
 QY 624 CACCGAGCTCAAAACCAACAGCAGACAGAAATGTATCATCCAAAGATCAGGACGAGTAACA 683  
 Db 184 HisProSerThrAspGlnGlnThrAsnLeuTyrValGlnAlaSerGlyArgValThr 203  
 QY 684 GTCTCAACAAAAGAGTCAACAAAGATAGTCCCTTAATATCGGATCTAGACCGTGGTT 743  
 Db 204 ValSerThrLysArgSerGlnGlnThrIleProAsnIleGlySerArgProTrpVal 223  
 QY 744 AGCGGTCAATCAGGAGGAGTAACTATATCTGACCATTTGTAACCTGAGATATCTTA 803  
 Db 224 ArgGlyLeuSerSerArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeu 243  
 QY 804 ATGATAAACAGTAATGGCACTTAGTTGACCGCGGGATATTTTAAATTTGAAACACAGG 863  
 Db 244 ValIleAsnSerAsnGlyAsnLeuIleAlaProArgGlyTyrPheLysMetArgThrGly 263  
 QY 864 AAAGCTCTGTAATGAGATCAGATGACACCATAGACATTTGTCTGTAATGTATTACA 923  
 Db 264 LysSerSerIleMetArgSerAspAlaProIleGlyThrCysIleSerGluCysIleThr 283  
 QY 924 CAAATGGAAGCATCCCAACGACAAACCATTTTCAAAATGTGAACAAAGTTTACATATGA 983  
 Db 284 ProAsnGlySerIleProAsnAspLysProPheGlnAsnValAsnLysIleThrTyrGly 303  
 QY 984 AAATGCCCAAGTATATATCAGGCAAAACACTTTTAAAGCTGGCCACTGGGATGAGGAATATA 1043  
 Db 304 AlaCysProLysTyrValLysGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnVal 323  
 QY 1044 CCAGAAACCAATCAGA 1061  
 Db 324 ProGluLysGlnThrArg 329  
 RESULT 10  
 ABP53895  
 ID ABP53895 standard; protein; 363 AA.  
 XX  
 AC ABP53895;  
 DT 07-JAN-2003 (first entry)  
 XX  
 DE Influenza A virus (A/Bangkok/1/79) haemagglutinin partial protein.  
 XX  
 KW Influenza; Influenza A virus; pathogenicity; RNA viral disease;  
 KW viral infection; selenium; vaccine; virucide; anti-HIV.  
 XX  
 OS Influenza A virus.  
 XX  
 PN WO200278717-A2.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 26-MAR-2002; 2002WO-EP003025.  
 XX  
 PR 28-MAR-2001; 2001US-00819387.  
 XX  
 PA (NEST ) SOC PROD NESTLE SA.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 XX  
 PI Beck M, German B, Levander O, Van Dael P;  
 XX  
 DR WPI; 2002-759948/82.  
 DR N-PSDB; ABQ82724.  
 XX  
 PT Treatment of influenza or reducing the risk of contracting influenza  
 PT involves administering selenium to an individual.  
 XX  
 PS Example 1; Page; 31pp; English.

XX The present invention describes a method for treating influenza or  
 CC reducing the risk of contracting influenza, which involves administering  
 CC selenium to an individual. Also described is a method for enhancing the  
 CC efficacy of a viral vaccine by administering an antioxidant, preferably  
 CC selenium, to an individual receiving the viral vaccine. The method can be  
 CC used for treating influenza, for reducing the risk of contracting  
 CC influenza, and for enhancing the efficacy of viral vaccine (preferably  
 CC influenza vaccine) in an infant, elderly, a patient or a pet. It can also  
 CC be used for treating virus such as coxsackie and HIV virus. The method  
 CC provides an improved treatment for viral infection, by reducing in vivo  
 CC mutations of the RNA virus. The method also improves a vaccine used to  
 CC prevent transmission of an RNA viral disease. The present sequence  
 CC represents the haemagglutinin protein from Influenza A virus  
 CC (A/Bangkok/1/79). N.B. The present sequence is not given in the  
 CC specification, but is taken from the Genbank accession number AF201843,  
 CC as specified on page 7  
 XX

SQ Sequence 363 AA;  
 Alignment Scores:  
 Pred. No.: 5,83e-139 Length: 363  
 Score: 1475.50 Matches: 268  
 Percent Similarity: 88.70% Conservative: 38  
 Best Local Similarity: 77.68% Mismatches: 38  
 Query Match: 77.17% Indels: 1  
 Ds: 5 Gaps: 1

US-10-826-929A-1 (1-1061) x ABP53895 (1-363)  
 QY 30 ATGAAGACAACCACTATTATTTGATCTACTGACCCATTTGGTCTACAGTCAAAAC---CCA 86  
 Db 1 MetLysThrIleAlaLeuSerTyrIleLeuCysLeuValPheAlaGlnAsnLeuPro 20  
 QY 87 ACCAGTGGAAACAACACAGCCACATTTATGTCTGGGACACCATGCTAGTACGAAATGGAACA 146  
 Db 21 GlyAsnAspAsnSerThrAlaThrLeuCysLeuGlyHisHisAlaValProAsnGlyThr 40  
 QY 147 TTGGTAAAAACAATACTGATGACCAAAATTCAGGTGACAAATGCTACTGAAATTTAGTTCTAG 206  
 Db 41 LeuValLysThrIleThrAsnAspGlnIleGluValThrAsnAlaThrGluLeuValGln 60  
 QY 207 AGCATTTTCAATAGGGAAATATGCAACAACTCATATAAAGTTTCTAGATGGAGAATTTGC 266  
 Db 61 SerSerSerThrGlyArgIleCysAspSerProHisArgIleLeuAspGlyLysAsnCys 80  
 QY 267 ACATTATAGATGCAATGCTAGGAGACCCCACTGTGTATGTCTTCCAGTATGAGAAATGG 326  
 Db 81 ThrLeuIleAspAlaLeuLeuGlyAspProHisCysAspGlyPheGlnAsnGluLysTrp 100  
 QY 327 GACCTCTTCATAGAAAGACGAGCGCTTTTCAGCAATTCCTACCCATATGACATCCCTGAC 386  
 Db 101 AspLeuPheValGluArgSerLysAlaPheSerAsnCysTyrProTyrAspValProAsp 120  
 QY 387 TATGATCGCTCCGGTCCATTGTAGCATCTCTCAGGAACATTAGAAATTCACAGCAGAGGA 446  
 Db 121 TyrAlaSerLeuArgSerLeuValAlaSerSerGlyThrLeuGluPheIleAsnGluGly 140  
 QY 447 TTCATATGACAGGTGTCTACTCAAAACCGAAGAGTGGAGCTGCAAAAGGGGATCAGCC 506  
 Db 141 PheAsnTrpThrGlyValThrGlnSerGlyGlySerTyrAlaCysLysArgGlySerAsp 160  
 QY 507 GATAGTTTCTTTAGCCGACTGAATTTGGCTAAACAAATCTGGAAACTCTTACCCACATTG 566  
 Db 161 LysSerPhePheSerArgLeuAsnTrpLeuTyrGluSerGluSerLysTyrProValLeu 180  
 QY 567 AATGTGACAATGCCCTTAAACAATAAATAATTCGACAAACTATATCATCTGGGGGATTCATCAC 626  
 Db 181 AsnValThrMetProAsnAsnGlyAsnPheAspLysLeuTyrIleTrpGlyValHis 200  
 QY 627 CCGAGCTCAAAACCAACAGCAGACAGAAATTTGATCCAAAGATCAGGACGAGTAAACAGTC 686  
 Db 201 ProSerThrAspLysGluGlnThrAsnLeuTyrValArgAlaSerGlyArgValThrVal 220

181 AsnValThrMetProAsnAsnAspPheAspLeuTyrIleTrpGlyValHis 200  
627 CCGAGTCAACCAACAGCAGACAGAAATGTACATCAAGATCAGACAGTAAACAGTC 686  
201 ProSerThrAspGlnGluThrSerLeuTyrValGlnAlaSerGlyArgValThrVal 220  
687 TCAACAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGTACG 746  
221 SerThrLysArgSerGlnThrIleProAsnIleGlySerArgProIrpValArg 240  
747 GGTCAATCAGCGCAGGATAGCATATCTGACCATTTGAAACCTGGAGATCTCTAATG 806  
241 GlyLeuSerSerArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuVal 260  
807 ATAAACAGTAATGGCACTAGTTGACCGCGGGATATTTAAATTTGAAACAGGAAA 866  
261 IleAsnSerAsnGlyAsnLeuIleAlaProArgGlyTyrPhenylsMetArgThrGlyLys 280  
867 AGCTCTGTAATGATCAGATCAGATCAGCCATAGACATTTGTCTGAATGTATTACACCA 926  
281 SerSerIleMetArgSerAspAlaProIleGlyThrCysIleSerGlyCysIleThrPro 300  
927 AATGGAAGCATCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACATATGAAAA 986  
301 AsnGlySerIleProAsnAspLysProPheGlnAsnValAsnLysIleThrTyrGlyAla 320  
987 TDCCCCAAGTATATCAGGAAACACTTTAAAGTCGGCCATCGGATAGGAATATACCA 1046  
321 CysProLysTyrValLysGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValPro 340  
1047 GAAACCAATCAGA 1061  
341 GluLysGlnThrArg 345

RESULT 9  
ADR89571  
ID ADR89571 standard; protein; 329 AA.  
XX AC ADR89571;  
XX  
XX 02-DEC-2004 (first entry)  
XX  
XX Influenza virus haemagglutinin.  
XX  
XX Influenza virus haemagglutinin; aptamer; vaccine; gene therapy; DNA immunisation;  
XX virucide.  
XX  
XX Influenza virus.  
XX  
XX Key Location/Qualifiers  
FT Region 91..261  
FT /note= "Region specifically referred to in Claim 105"  
FT Region 116..261  
FT /note= "Globular region, mediates binding to host cell  
FT determinants; this region is specifically referred to in  
FT Claim 106"  
FT Region 116..245  
FT /note= "Region specifically referred to in Claim 107"  
XX  
XX WO2004076621-A2.  
XX  
XX 10-SEP-2004.  
XX  
XX 24-FEB-2004; 2004WO-IL000182.  
XX  
XX 27-FEB-2003; 2003US-0449863P.  
XX  
XX (YEDA ) YEDA RES & DEV CO LTD.  
XX  
XX Arnon R, Jeon S, Kayhan B, Ben-Yedidia T;  
XX WPI; 2004-653392/63.  
XX  
XX DR

XX New nucleic acid molecule binding a polypeptide participating in  
PT influenza virus infection, useful for diagnosing or treating influenza  
PT virus infection in vertebrates such as avian, swine and humans.  
XX  
XX Claim 5; SEQ ID NO 1; 121pp; English.  
XX  
XX The present sequence is that of influenza virus haemagglutinin.  
XX Oligonucleotides (e.g. aptamers) designed to bind conserved sequences in  
XX the HA polypeptide can be used to prevent virus binding to host cells.  
XX Such aptamers can be used to diagnose and treat influenza virus infection  
XX in vertebrates such as avian, swine and humans. They exhibit viral cross-  
XX reactivity and as such can be used as universal vaccines against the  
XX influenza virus. A claimed nucleic acid molecule comprises a  
XX polynucleotide sequence capable of specifically binding a polypeptide  
XX participating in influenza virus infection of cells. The polypeptide is  
XX an influenza virus polypeptide such as HA or a host cell polypeptide such  
XX as a sialic acid receptor. The nucleic acid molecule is single-stranded  
XX DNA or RNA, e.g. A21 ADR89581 or A22 ADR89582. It is preferably capable  
XX of binding to amino acids 91-261 of the present HA sequence. A claimed  
XX method of generating a molecule capable of inhibiting influenza virus  
XX infection comprises: contacting a plurality of nucleic acid molecules  
XX with a polypeptide participating in influenza virus infection of cells,  
XX e.g. HA; and identifying nucleic acid molecule(s) capable of specifically  
XX binding the polypeptide. The nucleic acid is used in claimed methods of:  
XX treating or preventing influenza virus infection; identifying influenza  
XX virus in a biological sample; and targeting an antiviral agent to an  
XX influenza virus-infected tissue. A claimed polypeptide useful for  
XX vaccination against influenza virus comprises amino acids 91-261, 116-261  
XX or 116-245 of the present HA sequence.  
XX  
XX Sequence 329 AA;

Alignment Scores:  
Pred. No.: 9.86e-141 Length: 329  
Score: 1493.00 Matches: 268  
Percent Similarity: 90.80% Conservative: 28  
Best Local Similarity: 82.21% Mismatches: 30  
Query Match: 78.09% Indels: 0  
DB: Gaps: 0  
US-10-826-929A-1 (1-1061) x ADR89571 (1-329)  
QY 84 CCAACCCAGTGGAAACAACACAGCCACATTTCTGGGACACCATGAGCAATGCA 143  
DB 4 ProGlyAsnAspAsnSerThrAlaThrLeuCysLeuGlyHisAlaValProAsnGly 23  
QY 144 ACATTGGTAAACAAATACTGATGACCAAAATGGAGTGACAAATGCTACTGATTT 203  
DB 24 ThrLeuValLysThrIleThrAsnAspGlnIleGluValThrAsnAlaThrGluLeuVal 43  
QY 204 CAGAGCATTTCAATAGGNAATATGCAACACTCATATAAGTTCTAGATGGAAGAAAT 263  
DB 44 GlnSerSerThrGlyLysIleCysAsnAsnProHisGlyLeuAspGlyIleAsn 63  
QY 264 TGCACATAATAGATGCAATGCTAGGAGACCCCTGAGTGTCTTCCAGTATGAGAAT 323  
DB 64 CysThrLeuIleAspAlaLeuLeuGlyAspProHisCysAspGlyPheGlnAsnGluThr 83  
QY 324 TGGGACCTCTTCATAGAAAGAGCAGCGCTTTTTCAGCAATTTGTCATCATATGATCCCT 383  
DB 84 TrpAspLeuPheValGluArgSerLysAlaPheSerAsnCysTyrProTyrAspValPro 103  
QY 384 GACTATGATCCGCTCCGTCATTTAGCATCTCAGGAACATTTAGAAATTCACAGCAGAG 443  
DB 104 AspTyrAlaSerLeuArgSerLeuValAlaSerSerGlyThrLeuGluPheIleAsnGlu 123  
QY 444 GGATTACATGACAGAGTGTCTCACTCAAAACGGAAGAGTGGAGCTTCGAAAGGGGATCA 503  
DB 124 GlyPheThrTrpThrGlyValThrGlnAsnGlyGlySerAsnAlaCysLysArgGlyPro 143  
QY 504 GCCGATAGTTCTTTAGCCGACTGATTTGGCTTAAACAAATCTGGAAACTCTTACCCACA 563  
DB

```

Db 121 TyrAlaSerLeuArgSerLeuValAlaSerSerGlyThrLeuGluPheIleSerGluGly 140
QY 447 TTCACATGACAGAGTGTCACTCAAAACGGAAGAGTGGAGCTGCAAAAGGGGATCAGCC 506
Db 141 PheThrTrpThrGlyValThrGlnAsnGlyGlySerAsnAlaCysLysArgGlyProAsp 160
QY 507 GATAGTTCTTTAGCCGACTGAATTTGGCTTAACAAATCTGGAACCTCTTACCCCAATG 566
Db 161 SerGlyPhePheSerArgLeuAsnTrpLeuTyLysSerGlySerThrTyProValLeu 180
QY 567 AATGTGCAATGCTTAAACAAATTAATTCGACAACTATACATCTGGGGGATTCATCAC 626
Db 181 AsnValThrMetProAsnAsnAspAsnPheAspLysLeuTyLysLeuTrpGlyValHis 200
QY 627 CGGACTCAAACCAACAGCAGACAAATTTGTATCTCCAAAGATCAGGACGAGTAACTGC 686
Db 201 ProSerThrAspGlnGlnThrSerLeuTyValGlnAlaSerGlyArgValThrVal 220
QY 687 TCAACAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCTGGGTAGG 746
Db 221 SerThrLysArgSerGlnGlnThrIleProAsnIleGlySerArgProTrpValArg 240
QY 747 GGTCAATCAGGACGAGTATAGCATATCTGACCATTTGAACTGGAGATATCTTAATG 806
Db 241 GlyLeuSerSerArgIleSerIleTyTrpThrIleValLysProGlyAspIleLeuVal 260
QY 807 ATAAACAGTATGGCACTTAGTTCACCGCGGGATATTTAAATTAACAAACAGGAAA 866
Db 261 IleAsnSerAsnGlyAsnLeuIleAlaProArgGlyTyPheLysMetArgThrGlyLys 280
QY 867 AGCTCTGTAATCAGATCAGATGACCCATAGACATTTGTGTCTGTAATGTATTACACCA 926
Db 281 SerSerIleMetArgSerAspAlaProIleGlyThrCysIleSerGluCysIleThrPro 300
QY 927 AATGAAGCATCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACATATGAAA 986
Db 301 AsnGlySerIleProAsnAspLysProPheGlnAsnValAsnLysIleThrTyGlyAla 320
QY 987 TCCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACCA 1046
Db 321 CysProLysTyValLysGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValPro 340
QY 1047 GAAAGCAAAATCAGA 1061
Db 341 GlyLysGlnThrArg 345

```

## RESULT 8

```

ABB05774
ID ABB05774 standard; protein; 566 AA.
XX AC ABB05774;
XX DT 07-MAY-2002 (first entry)
XX DE Influenza A/Udorn/72 (H3N2) Strain HA protein SEQ ID NO:22.
XX KW Influenza A/Udorn/72 (H3N2) strain; Influenzavirus A; diagnosis;
XX KW Influenza A virus; genome.
XX OS Influenzavirus A.
XX PN WO200200884-A2.
XX PD 03-JAN-2002.
XX PF 21-JUN-2001; 2001WO-US019826.
XX PR 23-JUN-2000; 2000US-0213650P.
XX PA (AMCY) AMERICAN CYANAMID CO.
XX PI Galarza JM, Latham TE;

```

```

XX WPI; 2002-139923/18.
DR N-PSDB; ABA93944.
XX PT Polynucleotide encoding complete sequence of Influenza A/Udorn/72 and
PT polypeptide, useful in diagnosis and for generating new influenza A
variant strains.
XX PS Disclosure; Page 83-85; 103pp; English.
XX CC The present invention describes an isolated polynucleotide (I) having the
CC complete sequence of the Influenza A/Udorn/72 (H3N2) strain in positive
CC strand, antigenomic message sense. ABA93934 to ABA93944 encode the
CC Influenza A/Udorn/72 (H3N2) strain proteins given in ABB05764 to ABB05774
CC from the present invention. (I) is useful for designing polymerase chain
CC reaction (PCR) primers for use in a PCR assay to detect the presence of
CC the corresponding virus segment in a sample or for designing and
CC selecting peptides for use in an enzyme linked immunosorbent assay to
CC detect the presence of the corresponding protein produced by that segment
CC in a sample, hence is useful in diagnosis and may be modified by mutation
CC to generate new influenza A variant strains. ABA94945 to ABA94039
CC represent Influenza A/Udorn/72 (H3N2) strain sequencing primers, which
CC are used in an example from the present invention
XX SQ Sequence 566 AA;
Alignment Scores:
Pred. No.: 1,31e-141 Length: 566
Score: 1502.50 Matches: 274
Percent Similarity: 88.70% Conservative: 32
Best Local Similarity: 79.42% Mismatches: 1
Query Match: 78.58% Indels: 1
DB: 5 Gaps: 1
US-10-826-929A-1 (1-1061) x ABB05774 (1-566)
QY 30 ATGAAGCAACCATTTTTCATCTACTGACCCATCGGTCTACAGTCAAAAC---CCA 86
Db 1 MetLysThrIleIleAlaLeuSerTyIlePheCysLeuValLeuGlyGlnAspPhePro 20
QY 87 ACCAGTGGAAACAACAGCCACCATTTATGTCGGGACACCATGAGTAGCAATGAACA 146
Db 21 GlyAsnAspAsnSerThrAlaThrLeuCysLeuGlyHisAlaValProAsnGlyThr 40
QY 147 TTGGTAAACAACTAATGATGACCAATTCAGGTGACAAATGCTTACTGAAATTTAGTTCAG 206
Db 41 LeuValLysThrIleThrAsnAspGlnIleGluValThrAsnAlaThrGluLeuValGln 60
QY 207 AGCATTTCAATAGGAAATATGCAACAACTCATATATAAAGTTCTAGATGGAGAAATGCG 266
Db 61 SerSerSerThrGlyLysIleCysAsnAsnProHisArgIleLeuAspGlyIleAspCys 80
QY 267 ACATTATAGATGCAATGCTAGGAGACCCCTGATGCTCTTCCAGTATCAGAAATGG 326
Db 81 ThrLeuIleAspAlaLeuLeuGlyAspProHisCysAspGlyPheGlnAsnGluThrTrp 100
QY 327 GACTCTTCTATAGAAAGACAGCGCTTTACGCAATTCCTACCCATATGACATCCCTGAC 386
Db 101 AspLeuPheValGluArgSerLysAlaPheSerAsnCysTyProTyAspValProAsp 120
QY 387 TATGATCGCTCCGGTCCATTTAGCATCTCTCAGAACATTAAGAATTACACAGCAGAGGA 446
Db 121 TyrAlaSerLeuArgSerLeuValAlaSerSerGlyThrLeuGluPheIleSerGluGly 140
QY 447 TTCACATGACAGGTGTCACCTCAAAACGGAAGAGTGGAGCTGCAAAAGGGGATCAGCC 506
Db 141 PheThrTrpThrGlyValThrGlnAsnGlyGlySerAsnAlaCysLysArgGlyProAsp 160
QY 507 GATAGTTCTTTAGCCGACTGAATTTGGCTTAACAAATCTGGAACCTCTTACCCCAATG 566
Db 161 SerGlyPhePheSerArgLeuAsnTrpLeuTyLysSerGlySerThrTyProValLeu 180
QY 567 AATGTGCAATGCTTAAACAAATTAATTCGACAACTATACATCTGGGGGATTCATCAC 626

```



```

QY 330 CTCCTCATAGAAAGAGCAGCGCTTTGACGAATTCCTACCCATATGACATCCCTGACTAT 389
Db |||||
QY 101 LeuPheIleGluArgSerSerAlaPheSerAsnCysTyrProTyrAspIleProAspTyr 120
Db |||||
QY 390 GCATCGCTCCGGTCCATTGTAGTACCTCTCAGGAACATTAGAAATTCACAGCAGAGGATTC 449
Db |||||
QY 121 AlaserLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140
QY 450 ACATCGACAGGTGTCTCACTCAAAACGAGAGAGTGGAGCTCGAAAGGGGATCAGCCCAT 509
Db |||||
QY 141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysArgGlySerAlaAsp 160
QY 510 AGTTCTTTAGCCGACTGAATGGCTAAACAAATCTGGAATCTTACCCACATTTGAAT 569
Db |||||
QY 161 SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyrProThrLeuAsn 180
QY 570 GTGACAAATGCTTAAACAAATTTTCGACAAACTATACATCTGGGGGATTCATCACCAG 629
Db |||||
QY 181 ValThrMetProAsnAsnAsnPheAspLysLeuTyrIleTrpGlyIleHisPro 200
QY 630 AGCTCAAACCAACAGACAGCAAAATTTGTACATCCAAAGATCAGACGAGTAACTCTCA 689
Db |||||
QY 201 SerThrAsnAsnGluGlnThrLysLeuTyrValGlnGluLeuGlyArgValThrValSer 220
QY 690 ACAAAAAGAGTCAACAAACGATAGTCCCTTAATATCGGATCTAGACCGTGGGTAGGGGT 749
Db |||||
QY 221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProGlyValArgGly 240
QY 750 CAATCAGGAGGATAGCATATCTGACCATTTGTAACCTGGAGATATCTTAATGATA 809
Db |||||
QY 241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle 260
QY 810 AACAGTATGCAACTAGTTCACCGCGGGGATATTTAAATTCGAAACAGGGAAGC 869
Db |||||
QY 261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysMetArgThrGlyLysSer 280
QY 870 TCTGTAATGAGATCAGATGACCCCATAGACATTTGTGTCTGTAATGTATTACACCAAT 929
Db |||||
QY 281 SerIleMetArgSerAspAlaProIleAspThrCysValSerGluCysIleThrProAsn 300
QY 930 GGAACATCCCAACAGACAAACATTTCAAAATGTGAACAAAGTTACATATGGAATGCG 989
Db |||||
QY 301 GlySerIleProAsnAspLysProGlnAsnValAsnLysValThrTyrGlyLysCys 320
QY 990 CCCAGTATATCAGCAAAACACTTTAAAGCTGGCCACTGGGATCAGGAATATACAGAA 1049
Db |||||
QY 321 ProLysTyrIleLysGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu 340
QY 1050 AAGCAATCAGA 1061
Db |||||
QY 341 LysGlnIleArg 344
RESULT 6
AAR63590
ID AAR63590 standard; protein; 566 AA.
XX
AC AAR63590;
XX
DT 25-MAR-2003 (revised)
DT 23-JUN-1995 (first entry)
XX
DE Full length H3N2 influenza A virus, strain A2/Aichi/2/68 HA protein.
XX
KW Conserved peptide; stem region; hemagglutinin; HA; H1N1; H2N2; PCR;
KW subtype; human; influenza A virus; immunogenic artificial peptide;
KW antigen; vaccine; infection; polymerase chain reaction; primer; amplify;
KW C179; region A; region B.
XX
OS Influenza A virus.
XX
FH Key Location/Qualifiers
FT Peptide 1..16
/note= "Signal peptide"

```

```

FT Domain 17..70
/note= "Stem region in N-terminal domain"
FT Domain 71..289
/note= "Globular head domain"
FT Domain 290..566
/note= "Stem region in C-terminal domain"
FT Peptide 334..338
/note= "Conserved region A'"
FT Peptide 392..403
/note= "Conserved region B'"
XX
PN EP621339-A2.
XX
PD 26-OCT-1994.
XX
PF 20-APR-1994; 94EP-00302819.
XX
PR 20-APR-1993; 93JP-00115216.
PR 16-MAR-1994; 94JP-00070194.
XX
PA (TAKI ) TAKARA SHUZO CO LTD.
XX
PI Okuno Y, Isegawa Y, Sasao F, Ueda S;
XX
WPI; 1994-325949/41.
N-PSDB; AAQ72855.
Human influenza-A virus haemagglutinin polypeptide(s) - useful in
influenza-A vaccine composition;
Example 2; Page 54-58; 68pp; English.
XX
The cDNA encoding this sequence was amplified using the primer sequences
given in AAQ72852-54 and this sequence represents the full length
hemagglutinin (HA) protein gene of the H3N2 subtype of human influenza A
virus, strain A2/Aichi/2/68. This full length protein contains two
conserved regions, the A' region, TGMNR and the B region,
QINGKLMR(I/V)IEK. These regions are close to each other in the stem of
the HA molecule and they represent epitopes which are recognised by the
antibody C179. C179 binds to the stem region of the HA molecule and thus
inhibits the membrane fusion action of the HA molecule and neutralises
the virus. Polypeptide molecules which contain the conserved peptide
regions, A and B, esp. HA molecules lacking the globular head region (see
also AAR63591), are antigenically equivalent to the stem region of the HA
molecule of influenza A virus. These artificial peptides may be used as
vaccines for prophylaxis of influenza A virus infection. (Updated on 25-
MAR-2003 to correct PN field.)
XX
SQ Sequence 566 AA;
Alignment Scores:
Pred. No.: 4,04e-144 Length: 566
Score: 1527.50 Matches: 277
Percent Similarity: 88.99% Conservative: 30
Best Local Similarity: 80.29% Mismatches: 37
Query Match: 79.89% Indels: 1
DB: 2 Gaps: 1
US-10-826-929A-1 (1-1061) x AAR63590 (1-566)
QY 30 ATGAAGACACCACTATTATTGATCTACTGACCCCATGGTCTACAGTCAAAAC---CCA 86
Db 1 MetLysThrIleAlaLeuSerTyrIlePheCysLeuAlaLeuGlyGlnAspLeuPro 20
QY 87 ACCAGTGAACAACACAGCCACATATTATGCTGGACACACCATGACAGTAGCAATGCAACA 146
Db 21 GlyAsnAspAsnSerThrAlaThrLeuCysLeuGlyHisAlaValProAsnGlyThr 40
QY 147 TTGGTAAAAACAATAACTGATGACCAAAATTCAGGTCACAAATGCTACTGAATTAGTTTCAG 206
Db 41 LeuValLysThrIleThrAspGlnIleGluValThrAsnAlaThrGluLeuValGln 60
QY 207 AGCATTTCAATAGGGGAAAATATGCAACAACTCATATAAAGTTCTTAGATGGAAAGAAATTC 266

```



```
DB:                2                0                Gaps:
US-10-826-929A-1 (1-1061) x AAR04943 (1-565)

QY 30 ATGAGACACACCATTTATTTGTTACTACTGACCCATTGGTCTACAGTCACCAACCAACC 89
Db 1 MetLysThrThrIleLeuLeuThrHisTrpValTySerGlnAsnProThr 20

QY 90 AGTGAACAAACACACGACCATTTATGTCTGGGACACCATGTCAGTAGCAAAATGGAACATTG 149
Db 21 SerGlyAsnAsnThrAlaThrLeuGlyHisAlaValAlaAsnGlyThrLeu 40

QY 150 GTAAAAACAATACTGATGACCAAAATGAGGTGACAAATGCTACTGAAATAGTTTCAGAGC 209
Db 41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60

QY 210 ATTTCAATAGGAAAATATGCAACACTCATATTAAGTTCTAGATGGAGAAATTCACACA 269
Db 61 ThrSerIleGlyIleCysAsnAsnProTyrArgValLeuAspGlyArgAsnCysThr 80

QY 270 TTAATAGATGCAATCTAGGACACCCCACTGTGTATGCTCTCCAGTATGAGAAATGGGAC 329
Db 81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyGluAsnTrpAsp 100

QY 330 CTCTTCATAGAAAGACGCGCTTTCAGCAATTCCTACCCATATGACATCCCTGACTAT 389
Db 101 LeuPheIleGluArgSerSerAlaPheSerAsnCysTyrProTyrAspIleProAspTyr 120

QY 390 GCATCGCTCCGCTCATTTGTAGCATCTTCAGGAACATTAGATTTACAGCAGAGGATTC 449
Db 121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140

QY 450 ACATGACACAGGTGTCACTCAAAACGGAAGTGGAGCTGCAAAAGGGATCAGCCGAT 509
Db 141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysArgArgGlySerAlaAsp 160

QY 510 AGTTCTTTAGCGACTGAATTTGGTAAACAAATCTGGAACCTTTACCCCACTTGAAT 569
Db 161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProThrLeuAsn 180

QY 570 GTGACAAATGCTTAACAATAAATTTGCAAACTATACATCTGGGGATTCATCACCAG 629
Db 181 ValThrMetProAsnAsnAsnPheAspLysLeuTyrIleTrpGlyIleHisPro 200

QY 630 AGCTCAAAACACAGACACAAATTTGATCCCAAGATCAGGACGAGTAACTCTCA 689
Db 201 SerThrAsnAsnGluGlnThrLysLeuTyrIleGlnGluSerGlyArgValThrValSer 220

QY 690 ACAAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGGTAGGGGT 749
Db 221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProTrpValArgGly 240

QY 750 CAATCAGCAGGATAGCATATATCTGACCATTTGAAACCTGGAGATATCTATATGATA 809
Db 241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle 260

QY 810 AACAGTAAATGGAACCTTAGTTCACCGGGGATATTTAAATTCGAAACAGGAAAGC 869
Db 261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysMetArgThrGlyLysSer 280

QY 870 TCTGTAATGAGATCAGATGACCCCATAGACATTTGTGTCTGTAATGTATTACACAAAT 929
Db 281 SerValMetArgSerAspAlaProIleAspThrCysValSerGluCysIleThrProAsn 300

QY 930 GGAAGCATCCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACATATGGAATGC 989
Db 301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrglyLysCys 320

QY 990 CCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATCAGGAATATACAGAA 1049
Db 321 ProLysTyrIleLysGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGly 340

QY 1050 AAGCAATCAGA 1061
```

```
|||||
Db 341 LysGlnIleArg 344

RESULT 4
AAP70711
ID AAP70711 standard; protein; 565 AA.
XX
AC AAP70711;
XX
DT 08-MAR-1991 (first entry)
XX
DE Equine influenza virus strain H3N8 (HIV-A2) haemagglutinin H3 gene product.
DE
KW HA; vaccine; Vaccina.
XX
OS Equine influenza virus.
XX
FH Key Location/Qualifiers
FT Protein 17..343
FT Protein /label= HA 1 protein
FT Protein 345..565
FT Protein /label= HA 2 protein
XX
PN W08607593-A.
XX
PD 31-DEC-1986.
XX
PF 20-JUN-1986; 86WO-US001343.
XX
PR 20-JUN-1985; 85US-00747020.
XX
PI (BIOT-) BIOTECHN RES PARTNE.
XX
PI Dale B, Cordell B;
XX
DR WPI; 1987-007191/01.
XX
DR N-PSDB; AAN71067.
XX
PT Preventing equine influenza virus infection - using recombinant vaccines produced using DNA sequences encoding haemagglutinin and neuraminidase glycoproteins.
PS Disclosure; Fig 2; 63pp; English.
XX
CC Peptides derived from the haemagglutinin H7 and H3 and neuraminidase N7 and N8 genes may be used to derive antigenic peptides useful in CC vaccination against equine influenza virus infection. Abs raised to the CC peptides may be used in diagnosis of the infection and construction of CC probes to mutated forms of the virus
XX
SQ Sequence 565 AA;

Alignment Scores:
Pred. No.: 1,766-168 Length: 565
Score: 1770.00 Matches: 327
Percent Similarity: 97.9% Conservative: 10
Best Local Similarity: 95.06% Mismatches: 7
Query Match: 92.57% Indels: 0
DB: 1 Gaps: 0

US-10-826-929A-1 (1-1061) x AAP70711 (1-565)

QY 30 ATGAGACACACCATTTATTTGTTACTACTGACCCATTGGTCTACAGTCACCAACCAACC 89
Db 1 MetLysThrThrIleLeuLeuThrHisTrpValTySerGlnAsnProThr 20

QY 90 AGTGAACAAACACACGACCATTTATGTCTGGGACACCATGTCAGTAGCAAAATGGAACATTG 149
Db 21 SerGlyAsnAsnThrAlaThrLeuGlyHisAlaValAlaAsnGlyThrLeu 40

QY 150 GTAAAAACAATACTGATGACCAAAATGAGGTGACAAATGCTACTGAAATAGTTTCAGAGC 209
Db 41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60

QY 210 ATTTCAATAGGAAAATATGCAACACTCATATTAAGTTCTAGATGGAGAAATTCACACA 269
Db 61 ThrSerIleGlyIleCysAsnAsnProTyrArgValLeuAspGlyArgAsnCysThr 80

QY 270 TTAATAGATGCAATCTAGGACACCCCACTGTGTATGCTCTCCAGTATGAGAAATGGGAC 329
Db 81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyGluAsnTrpAsp 100

QY 330 CTCTTCATAGAAAGACGCGCTTTCAGCAATTCCTACCCATATGACATCCCTGACTAT 389
Db 101 LeuPheIleGluArgSerSerAlaPheSerAsnCysTyrProTyrAspIleProAspTyr 120

QY 390 GCATCGCTCCGCTCATTTGTAGCATCTTCAGGAACATTAGATTTACAGCAGAGGATTC 449
Db 121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140

QY 450 ACATGACACAGGTGTCACTCAAAACGGAAGTGGAGCTGCAAAAGGGATCAGCCGAT 509
Db 141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysArgArgGlySerAlaAsp 160

QY 510 AGTTCTTTAGCGACTGAATTTGGTAAACAAATCTGGAACCTTTACCCCACTTGAAT 569
Db 161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProThrLeuAsn 180

QY 570 GTGACAAATGCTTAACAATAAATTTGCAAACTATACATCTGGGGATTCATCACCAG 629
Db 181 ValThrMetProAsnAsnAsnPheAspLysLeuTyrIleTrpGlyIleHisPro 200

QY 630 AGCTCAAAACACAGACACAAATTTGATCCCAAGATCAGGACGAGTAACTCTCA 689
Db 201 SerThrAsnAsnGluGlnThrLysLeuTyrIleGlnGluSerGlyArgValThrValSer 220

QY 690 ACAAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGGTAGGGGT 749
Db 221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProTrpValArgGly 240

QY 750 CAATCAGCAGGATAGCATATATCTGACCATTTGAAACCTGGAGATATCTATATGATA 809
Db 241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle 260

QY 810 AACAGTAAATGGAACCTTAGTTCACCGGGGATATTTAAATTCGAAACAGGAAAGC 869
Db 261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysMetArgThrGlyLysSer 280

QY 870 TCTGTAATGAGATCAGATGACCCCATAGACATTTGTGTCTGTAATGTATTACACAAAT 929
Db 281 SerValMetArgSerAspAlaProIleAspThrCysValSerGluCysIleThrProAsn 300

QY 930 GGAAGCATCCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACATATGGAATGC 989
Db 301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrglyLysCys 320

QY 990 CCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATCAGGAATATACAGAA 1049
Db 321 ProLysTyrIleLysGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGly 340

QY 1050 AAGCAATCAGA 1061
```

CC particularly horses. The present sequence is a wild type equine influenza  
 CC virus H3N8 haemagglutinin (HA) protein denoted as PeiWtHA565. This  
 CC sequence is modified to generate cold-adapted equine influenza virus  
 XX  
 SQ Sequence 565 AA;

## Alignment Scores:

Pred. No.: 3,466-170 Length: 565  
 Score: 1787.00 Matches: 333  
 Percent Similarity: 99.42% Conservative: 9  
 Best Local Similarity: 96.80% Mismatches: 2  
 Query Match: 93.46% Indels: 0  
 DB: 3 Gaps: 0

US-10-826-929A-1 (1-1061) x AAY70056 (1-565)

QY 30 ATGAGACAAACATTATTGTTGATCTACTACCCATGGTCTACAGTCACAAACCAACC 89  
 DB 1 MetLysThrThrIleLeuLeuLeuProLeuThrHisTrpValTy-SerGlnAsnProThr 20  
 QY 90 AGTGGAAACAACACAGCCACATTATGCTGGACACCATGTCAGTAGCAAAATGCAATG 149  
 DB 21 SerGlyAsnAsnThrAlaThrLeuLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40  
 QY 150 CTAAACAACTAACTGATGACCAAAATGAGGTGACAAATGCTACTGAATTAGTTGAGGC 209  
 DB 41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60  
 QY 210 ATTTCATAGGGAATAATATGCAACAACTCATATATAAATCTAGATGGAATAATGCCA 269  
 DB 61 IleSerIleGlyLysIleCysAsnAsnSerTyArgValLeuAspGlyArgAsnCysThr 80  
 QY 270 TTAATAGATCAATGTAGAGACCCCACTGTGATGCTCTCCAGTATGAGATTGGGAC 329  
 DB 81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyArgLysAsnTrpAsp 100  
 QY 330 CTCTCATAGAAAGACAGCGCTTTGAGCAATGCTACCCATATGACATCTCCCTGACTAT 389  
 DB 101 LeuPheIleGluArgSerSerAlaPheSerSerCysTyProTyAspIleProAspTy 120  
 QY 390 GCATCGCTCCGTPCCATTGTAGCATCTCAGGACATTAAGAAATTCACAGAGGGATTTC 449  
 DB 121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140  
 QY 450 ACATGACAGCTGTCTCAATAAATTCGACAAATTCGACAACTATACATCTGGGGATTCTACCCG 509  
 DB 141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlySerCysLysArgGlySerAlaAsp 160  
 QY 510 AGTTCTTTAGCCGACTGAATTCGCTAAACAAATCTGGAACCTCTTACCCCACTTGAAT 569  
 DB 161 SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyProThrLeuAsn 180  
 QY 570 GTCACAAATGCTCAATAAATTCGACAAATTCGACAACTATACATCTGGGGATTCTACCCG 629  
 DB 181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyIleTrpGlyIleHisHisPro 200  
 QY 630 AGCTCAACCAACAGCAGACAGATGTCATACCAAGATTCAGACAGTAAACAGTCTCA 689  
 DB 201 SerSerAsnLysGluGlnThrLysLeuTyIleGlnGluSerGlyArgValThrValSer 220  
 QY 690 ACAAAGAAGTCAACAAACATAGTCCCTAATATCGATTCGATCGATCGGTGGGTAGGGT 749  
 DB 221 ThrLysArgSerGlnThrIleIleProAsnIleGlySerArgProArgValArgGly 240  
 QY 750 CANTCAGGAGGATAAGCATATATCTGACCATTTGTAACCTGGATATCTTAATGATA 809  
 DB 241 GlnSerGlyArgIleSerIleTyTrpIleValLysProGlyAspIleLeuMetIle 260  
 QY 810 AACAGTAAATGCACTTAGTTGACCGCGGGATATTTAAATTTGAAAAACAGGAAAGC 869  
 DB 261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyTrpPheLysLeuLysThrGlyLysSer 280  
 QY 870 TCTGTAATGATGATCAGATGACCCATAGACATTTGTGTGTCTGTAATGTTACACCAAT 929

Db 281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn 300  
 QY 930 GGAAGCATCCCAACAGCAAAACCATTTCAAATGTGAACAAAGTTACATATGGAATGC 989  
 Db 301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyGlyLysCys 320  
 QY 990 CCCAAGTATATCAGGCAAAACACATTAAAGCTGCCACTGGATGAGGAATATACCAAA 1049  
 Db 321 ProLysTyIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu 340  
 QY 1050 AAGCAAAATCAGA 1061  
 Db 341 LysGlnIleArg 344  
 RESULT 3  
 AAR04943  
 ID AAR04943 standard; protein; 565 AA.  
 XX AAR04943;  
 XX 25-MAR-2003 (revised)  
 DT 02-OCT-1990 (first entry)  
 XX Equine hemagglutinin H3 (EIV-A2).  
 XX Recombinant vaccines; equine influenza virus; haemagglutinin; H3;  
 KW neuraminidase; N8.  
 XX Equine influenza virus.  
 XX Key Location/Qualifiers  
 FT Region 102..1182  
 FT Region /label= N-terminal HA1 50kD portion  
 FT Region 1186..1748  
 FT /label= C-terminal HA2 27kD portion  
 XX US4920213-A.  
 XX 24-APR-1990.  
 XX 21-JUL-1986; 86US-00888250.  
 XX 20-JUN-1985; 85US-00747020.  
 XX (BIOT-) BIOTECH RES PARTNERS LTD.  
 XX Dale B, Cordell B;  
 XX WPI; 1990-163647/21.  
 DR P-PSDB; AAR04943.  
 XX Recombinant vaccines against equine influenza virus - produced using DNA  
 PT sequences encoding haemagglutinin and neuraminidase glyco-protein(s).  
 XX Disclosure; Page ?; 27pp; English.  
 XX There are nine neuraminidase (NA) subtypes and twelve haemagglutinin (HA)  
 CC subtypes. The strain carrying H3N8 glycoproteins is designated equine  
 CC influenza virus (EVI)-A2. The cDNA sequences will be useful in the  
 CC construction of diagnostic probes for the disease and of probes for  
 CC obtaining new cDNAs of the mutated form of the virus. Recombinant  
 CC vaccines are produced. See also AAR04596-Q04599. (Updated on 25-MAR-2003  
 CC to correct PA field.)  
 XX Sequence 565 AA;  
 SQ  
 Alignment Scores:  
 Pred. No.: 2,776-169 Length: 565  
 Score: 1778.00 Matches: 328  
 Percent Similarity: 98.26% Conservative: 10  
 Best Local Similarity: 95.35% Mismatches: 6  
 Query Match: 92.99% Indels: 0



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: February 27, 2005, 18:06:24 ; Search time 180 Seconds  
(without alignments)  
4559.475 Million cell updates/sec

Title: US-10-826-929A-1  
Perfect score: 1912  
Sequence: 1 agcaaaagcaggggatatatt.....taccgaaagcaaatcaga 1061

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues  
Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/cgn2\_1/USPTO.spool\_p/US10826929/runat\_27022005\_095242\_27576/app\_query.fasta\_1.1223  
-DB=A\_Geneseq\_16Dec04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCI=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi  
-LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFWT=ptp -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10826929@cgn\_1\_1224 @runat\_27022005\_095242\_27576 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A\_Geneseq\_16Dec04.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1794	93.8	565	3 AAY70057	Aay70057 Cold-adap
2	1787	93.5	565	3 AAY70056	Aay70056 Wild type
3	1778	93.0	565	2 AAR04943	Aar04943 Equine he
4	1770	92.6	565	1 AAP70711	Aap70711 Equine in
5	1760	92.1	565	2 AAW44946	Aaw44946 EIV Fonta
6	1527.5	79.9	566	2 AAR63590	Aar63590 Full leng
7	1507.5	78.8	566	5 ABB05767	Abb05767 Influenza
8	1502.5	78.6	566	5 ABB05774	Abb05774 Influenza
9	1493	78.1	329	8 ADR89571	Adr89571 Influenza
10	1475.5	77.2	363	5 ABP53895	Abp53895 Influenza

11	1472	77.0	386	1 AAP40615	Aap40615 Sequence
12	1449.5	75.8	550	5 ABP53894	Abp53894 Influenza
13	1442	75.4	329	5 ABP53897	Abp53897 Influenza
14	1436	75.1	329	5 ABP53896	Abp53896 Influenza
15	1427.5	74.7	566	2 AAW68406	Aaw68406 SIV strai
16	1421	74.3	570	2 AAW01669	Aaw01669 Influenza
17	1421	74.3	570	2 AAW75441	Aaw75441 Influenza
18	1421	74.3	570	4 AAE04951	Aae04951 Influenza
19	1404.5	73.5	571	2 AAW01673	Aaw01673 Influenza
20	1404.5	73.5	571	2 AAW75445	Aaw75445 Influenza
21	1404.5	73.5	571	4 AAE04955	Aae04955 Influenza
22	1398.5	73.1	571	2 AAW01676	Aaw01676 Influenza
23	1398.5	73.1	571	2 AAW75448	Aaw75448 Influenza
24	1398.5	73.1	571	4 AAE04958	Aae04958 Influenza
25	1373	71.8	347	5 AAU76670	Aau76670 Influenza
26	786	41.1	171	8 ADR89583	Adr89583 Influenza
27	664	34.7	146	8 ADR89584	Adr89584 Influenza
28	657	34.4	563	7 ADG43790	Adg43790 Influenza
29	645	33.7	564	5 AAO19499	Aao19499 Recombina
30	641	33.5	570	1 AAP70710	Aap70710 Equine in
31	641	33.5	570	1 AAR04940	Aar04940 Equine he
32	624.5	32.7	571	2 AAW55997	Aaw55997 Protein S
33	624.5	32.7	573	2 ADH29822	Adh29822 Swinepox
34	593	31.0	566	2 AAR08259	Aar08259 Haemagglu
35	593	31.0	566	8 ADL90068	Adl90068 A/PR/8 in
36	588	30.8	566	2 AAW68405	Aaw68405 SIV strai
37	585	30.6	130	8 ADR89585	Adr89585 Influenza
38	580.5	30.4	566	3 AAB29746	Aab29746 Influenza
39	580	30.3	572	2 AAW01670	Aaw01670 Influenza
40	580	30.3	572	2 AAW75442	Aaw75442 Influenza
41	580	30.3	572	4 AAE04952	Aae04952 Influenza
42	538.5	28.2	316	8 ADR90613	Adr90613 Influenza
43	536.5	28.1	412	7 ADJ91998	Adj91998 Influenza
44	528.5	27.6	216	8 ADR90614	Adr90614 Structure
45	521	27.2	562	2 AAR63588	Aar63588 Full leng

ALIGNMENTS

RESULT 1  
AAY70057  
ID AAY70057 standard; protein; 565 AA.

XX AAY70057;  
XX  
XX 05-JUN-2000 (first entry)  
XX Cold-adapted equine influenza virus H3N8 haemagglutinin protein.  
XX Haemagglutinin protein; modified HA protein; horse; cold-adaptation;  
KW reassortant virus; temperature sensitivity; dominant interference;  
KW attenuation; antiviral; vaccine; prevention; treatment;  
KW influenza A virus infection.  
XX  
XX Equine influenza virus H3N8.  
XX  
XX WO200009702-A1.  
XX  
XX 24-FEB-2000.  
XX  
XX 12-AUG-1999; 99WO-US018583.  
XX  
XX 13-AUG-1998; 98US-00133921.  
XX  
XX (UYPI-) UNIV PITTSBURGH.  
XX Dowling PW, Youngner JS;  
XX WPI; 2000-224339/19.  
XX N-PSDB; AA250976.  
XX  
XX New cold-adapted equine influenza viruses and reassortant viruses used as  
PT vaccines for treating influenza infections in animals, particularly

[illegible]

Db 961 ATGTGAACAAAGTTACATATGGAATGCCCCAGTATATATCAGGCAAAACACTTTTAAAGC 1020  
QY 1021 TGGCCACTGGGATGAGGAATATACAGAAAAGCAATCAGA 1061  
Db 1021 TGGCCACTGGGATGAGGAATGATACAGAAAAGCAATCAGA 1061  
RESULT 14  
AR343239  
LOCUS 1762 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 10 from patent US 6579528.  
ACCESSION AR343239  
VERSION AR343239.1 GI:33738757  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1762)  
AUTHORS Dowling, P.W. and Youngner, J.S.  
TITLE Cold-adapted equine influenza viruses  
JOURNAL Patent: US 6579528-A 10 17-JUN-2003;  
FEATURES Location/Qualifiers  
source 1..1762  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Query Match 97.4%; Score 1033.8; DB 6; Length 1762;  
Best Local Similarity 98.4%; Pred. No. 2.3e-235;  
Matches 1044; Conservative 0; Mismatches 17; Indels 0; Gaps 0;  
QY 1 AGCAAAAGCAGGGGATATTTCTGCAATCATGACGACCAACCAATTTTGTACTACTGCA 60  
Db 1 AGCAAAAGCAGGGGATATTTCTGCAATCATGACGACCAACCAATTTTGTACTACTGCA 60  
QY 61 CCCATTGGGTCTACAGTCAAAACCCCAACCCAGTGGGAAACACAGCCACATTTATGCTGG 120  
Db 61 CCCATTGGGTCTACAGTCAAAACCCCAACCCAGTGGGAAACACAGCCACATTTATGCTGG 120  
QY 121 GACACCATGCTAGTGAATGGAACATTTGGTGAATAAACAATGATGACCAAAATTTGAGG 180  
Db 121 GACACCATGCTAGTGAATGGAACATTTGGTGAATAAACAATGATGACCAAAATTTGAGG 180  
QY 181 TGCAAAATGCTACTGAAATTTAGTTTCAGAGCAATTTCAATAGGGGAAAATATGCAAACTCAT 240  
Db 181 TGCAAAATGCTACTGAAATTTAGTTTCAGAGCAATTTCAATAGGGGAAAATATGCAAACTCAT 240  
QY 241 ATAAAGTCTTAGATGGAAGAAATTCACATTAATAGATGCAATGATGAGAGACCCCACT 300  
Query Match 97.4%; Score 1033.8; DB 6; Length 1762;  
Best Local Similarity 98.4%; Pred. No. 2.3e-235;  
Matches 1044; Conservative 0; Mismatches 17; Indels 0; Gaps 0;  
QY 1 AGCAAAAGCAGGGGATATTTCTGCAATCATGACGACCAACCAATTTTGTACTACTGCA 60  
Db 1 AGCAAAAGCAGGGGATATTTCTGCAATCATGACGACCAACCAATTTTGTACTACTGCA 60  
QY 61 CCCATTGGGTCTACAGTCAAAACCCCAACCCAGTGGGAAACACAGCCACATTTATGCTGG 120  
Db 61 CCCATTGGGTCTACAGTCAAAACCCCAACCCAGTGGGAAACACAGCCACATTTATGCTGG 120  
QY 121 GACACCATGCTAGTGAATGGAACATTTGGTGAATAAACAATGATGACCAAAATTTGAGG 180  
Db 121 GACACCATGCTAGTGAATGGAACATTTGGTGAATAAACAATGATGACCAAAATTTGAGG 180  
QY 181 TGCAAAATGCTACTGAAATTTAGTTTCAGAGCAATTTCAATAGGGGAAAATATGCAAACTCAT 240  
Db 181 TGCAAAATGCTACTGAAATTTAGTTTCAGAGCAATTTCAATAGGGGAAAATATGCAAACTCAT 240  
QY 241 ATAAAGTCTTAGATGGAAGAAATTCACATTAATAGATGCAATGATGAGAGACCCCACT 300  
Db 241 ATAGAGTCTTAGATGGAAGAAATTCACATTAATAGATGCAATGATGAGAGACCCCACT 300  
QY 301 GTGATGCTTCAGTATGAGAAATTTGGGACCTCTTCATAGAAAGACGACGCTTTTCAGCA 360  
Db 301 GTGATGCTTCAGTATGAGAAATTTGGGACCTCTTCATAGAAAGACGACGCTTTTCAGCA 360  
QY 361 ATTGCTACCCATATGACATCCCTGACTATGATCGCTCCGCTCCATTTAGCATCCTCAG 420  
Db 361 GTTGCTACCCATATGACATCCCTGACTATGATCGCTCCGCTCCATTTAGCATCCTCAG 420  
QY 421 GAACATTAGAAATTCACAGCAGAGGGATTCACATGGAAGAGTGTCACTCAAAAACGGAAGAA 480  
Db 421 GAACATTAGAAATTCACAGCAGAGGGATTCACATGGAAGAGTGTCACTCAAAAACGGAAGAA 480  
QY 481 GTGGAGCTTGCAAAAAGGGATCGCCGATAGTTCTTTAGCCGACTGAATTTGGCTAACAA 540  
Db 481 GTGGATCTTGCAAAAAGGGATCAGCCGATAGTTCTTTAGCCGACTGAATTTGGCTAACAG 540  
QY 541 AATCTGGAACCTCTTACCCACATTTGAATGTGACATGCTTCAACATAAATAATTTTCGACA 600  
Db 541 AATCTGGAACCTCTTACCCACATTTGAATGTGACATGCTTCAACATAAATAATTTTCGACA 600  
QY 601 AACTATACATCTGGGGATTTTCATACCCGAGCTCAAAACCAACAGCAGACAGAAATTTGTACA 660

Db 601 AACTATACATCTGGGGATTTTCATACCCGAGCTCAAAACAAAGACGACAAATTTGTACA 660  
QY 661 TCCAGAAATCAGGACGAGTAACTCTCAACAAAAGAGTCAACAAAAGGATAGTCCCTTA 720  
Db 661 TCCAGAAATCAGGACGAGTAACTCTCAACAAAAGAGTCAACAAAAGGATAGTCCCTTA 720  
QY 721 ATATCGGATCTAGACCGTGGTGTAGGGTCAATCAGGAGGAGTAAGCATATATCTGACCA 780  
Db 721 ACATCGGATCTAGACCGTGGTGTAGGGTCAATCAGGAGGAGTAAGCATATATCTGACCA 780  
QY 781 TTGTAAAAACCTGGGATATCCTAATGATAAACAAGTAATGGCAACTTTAGTTGACCGCGGG 840  
Db 781 TTGTAAAAACCTGGGATATCCTAACGATAAACAAGTAATGGCAACTTTAGTTGACCGCGGG 840  
QY 841 GATATTTTAAATTTGAAAACAGGAAAGCTCTGTATGATGATCAGATGACCCCATAGACA 900  
Db 841 GATATTTTAAATTTGAAAACAGGAAAGCTCTGTATGATGATCAGATGACCCCATAGACA 900  
QY 901 TTTGTGCTCTGAATGATTACACCAATGGAAGCATCCCAACGACAAACCAATTTTCAA 960  
Db 901 TTTGTGCTCTGAATGATTACACCAATGGAAGCATCCCAACGACAAACCAATTTTCAA 960  
QY 961 ATGTGAACAAAGTTACATATGGAATGCCCAAGTATATCAGGCAAAACACTTTTAAAGC 1020  
Db 961 ATGTGAACAAAGTTACATATGGAATGCCCAAGTATATCAGGCAAAACACTTTTAAAGC 1020  
QY 1021 TGGCCACTGGGATGAGGAATATACAGAAAAGCAATCAGA 1061  
Db 1021 TGGCCACTGGGATGAGGAATATACAGAAAAGCAATCAGA 1061  
RESULT 15  
AR455506  
LOCUS 1762 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 10 from patent US 6685946.  
ACCESSION AR455506  
VERSION AR455506.1 GI:42690326  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1762)  
AUTHORS Dowling, P.W. and Youngner, J.S.  
TITLE Cold-adapted equine influenza viruses  
JOURNAL Patent: US 6685946-A 10 03-FEB-2004;  
FEATURES Location/Qualifiers  
source 1..1762  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Query Match 97.4%; Score 1033.8; DB 6; Length 1762;  
Best Local Similarity 98.4%; Pred. No. 2.3e-235;  
Matches 1044; Conservative 0; Mismatches 17; Indels 0; Gaps 0;  
QY 1 AGCAAAAGCAGGGGATATTTCTGCAATCATGACGACCAACCAATTTTGTACTACTGCA 60  
Db 1 AGCAAAAGCAGGGGATATTTCTGCAATCATGACGACCAACCAATTTTGTACTACTGCA 60  
QY 61 CCCATTGGGTCTACAGTCAAAACCCCAACCCAGTGGGAAACACAGCCACATTTATGCTGG 120  
Db 61 CCCATTGGGTCTACAGTCAAAACCCCAACCCAGTGGGAAACACAGCCACATTTATGCTGG 120  
QY 121 GACACCATGCTAGTGAATGGAACATTTGGTGAATAAACAATGATGACCAAAATTTGAGG 180  
Db 121 GACACCATGCTAGTGAATGGAACATTTGGTGAATAAACAATGATGACCAAAATTTGAGG 180  
QY 181 TGCAAAATGCTACTGAAATTTAGTTTCAGAGCAATTTCAATAGGGGAAAATATGCAAACTCAT 240  
Db 181 TGCAAAATGCTACTGAAATTTAGTTTCAGAGCAATTTCAATAGGGGAAAATATGCAAACTCAT 240  
QY 241 ATAAAGTCTTAGATGGAAGAAATTCACATTAATAGATGCAATGATGAGAGACCCCACT 300

Qy	241	ATAAAGTTCTAGATGGGAAGAAATTTGCACATTAATAGATGCAATCTGTAGGAGACCCCCACT	300
Db	241	ATAGAGTTCTAGATGGGAAGAAATTTGCACATTAATAGATGCAATCTGTAGGAGACCCCCACT	300
Qy	301	GTGATGTCTTCCAGTATGAGAAATTTGGGACCTCTTTCATAGAAAGAAGCAGCGCTTTTCAGCA	360
Db	301	GTGATGTCTTTCAGTATGAGAAATTTGGGACCTCTTTCATAGAAAGAAGCAGCGCTTTTCAGCA	360
Qy	361	ATTGCTACCCATATGACATCCCTGACTATGCATCGCTCCGGTCCATTTGTAGCATCTCTCAG	420
Db	361	GTGCTACCCATATGACATCCCTGACTATGCATCGCTCCGGTCCATTTGTAGCATCTCTCAG	420
Qy	421	GAACATTAGAAATTTACACAGCAGAGGGATTCACATGCGCAGGTGTCACTCAAAAACGGAGAA	480
Db	421	GAACATTGGAAATTTACACAGCAGAGGGATTCACATGCGCAGGTGTCACTCAAAAACGGAGAA	480
Qy	481	GTGGAGCTTCGAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAAATTTGGCTAACAA	540
Db	481	GTGGATCTTCGAAAAGGGATCAGCCGATAGTTTCTTTAGCCGACTGAAATTTGGCTAACAG	540
Qy	541	AATCTGGAAAATCTTTTACCCACATTTGAATGTGACAATGCGCTTAAACAATAAATAATTTGAC	600
Db	541	AATCTGGAAAATCTTTTACCCACATTTGAATGTGACAATGCGCTTAAACAATAAATAATTTGAC	600
Qy	601	AACATATACATCTGGGGATTCATCACCCGAGCTCAACACCAACGACGACAGAAATTTGTACA	660
Db	601	AACATATACATCTGGGGATTCATCACCCGAGCTCAACCAAAAGACGACAAAATTTGTACA	660
Qy	661	TCCAAAGATCAGGACGAGTAACAGTCTCAACAAAAAGAGTCAACAAACGATAGTCCCTTA	720
Db	661	TCCAAAGATCAGGACGAGTAACAGTCTCAACAAAAAGAGTCAACAAACATTAATCCCTTA	720
Qy	721	ATATCGGATCTAGACCGTGGGTATGGGGTCAATCAGCAGAGTAAGCATATATCTGGACCA	780
Db	721	ACATCGGATCTAGACCGTGGGTCAATCAGCAGAGTAAGCATATATCTGGACCA	780
Qy	781	TTGTAAAACTGGAGATATCTTAATGATAAACAGTAATGCGCAATTTAGTTGCAACCGCGGG	840
Db	781	TTGTAAAACTGGAGATATCTTAACGATAAACAGTAATGCGCAATTTAGTTGCAACCGCGGG	840
Qy	841	GATATTTTAAATTTGAAAACAGGGAAAAAGCTCTGTAAATGAGATCAGATGCAACCATAGACA	900
Db	841	GATATTTTAAATTTGAAAACAGGGAAAAAGCTCTGTAAATGAGATCAGATGCAACCATAGACA	900
Qy	901	TTTGTGTGTCGTAATGTATTTACACCAATCGAAGCATCCCAACGACAAACCAATTTCAA	960
Db	901	TTTGTGTGTCGTAATGTATTTACCAAAATGGAAGCATCCCCAACGACAAACCAATTTCAA	960
Qy	961	ATGTGAACAAAGTTTACATATGGAATAATGCCCAAGTATATCAGGCAAAACACTTTTAAAGC	1020
Db	961	ATGTGAACAAAGTTTACATATGGAATAATGCCCAAGTATATCAGGCAAAACACTTTTAAAGC	1020
Qy	1021	TGSCCACTGGGATGAGGAATATACCGAAAAGCAAAATCAGA	1061
Db	1021	TGSCCACTGGGATGAGGAATGTACCAAGAAAGCAAAATCAGA	1061

RESULT 13  
AR254631

AR254631	LOCUS	AR254631	1762 bp	DNA	linear	PAT 20-DEC-2002
	DEFINITION	Sequence 10 from patent US 6482414.				

AR254631

VERSION AR254631.1 GI:27303652

## KEYWORDS

**SOURCE** Unknown.

SOURCE	ORGANISM	UNKNOWN.
UNKNOWN.	UNKNOWN.	UNKNOWN.

UNCLASSIFIED.

REFERENCE 1 (bases 1 to 1762)

REFERENCE  
AUTHORS  
I (Dases I CO 1/82)  
Dowling, P. W. and Youngner, J. S.

**AUTHORS** DOWLING, P.W. and YOUNGNER, J.S.  
**TITLE** Cold-adapted equine influenza viruses

JOURNAL OF CORONARY CARE 10 19-NOV-2002: US 6482414-A

**JOURNAL**  
**FEATURES**  
**Patent:** US 6482414  
**Location:**

FEATURES	Location/
Source	1 1762

source

TTDQIEVNTATLWVSIISIGKICNNISYRVLDGRNCTLIDAMLGDHCDVFOYENWDLF  
IERSAFNSCYDIPDVASRSIVASSGTLEFTEAGFTWGTQNGRSKACRGSAD  
SFFSLNMLTKSGNSYPTLNTVPMNNKPNFKLYIWIHHPNSNQTKLYIOESGRVT  
VTKSSQOITIIENIGSRPWRVQSGRISITWTIVKPGDILMNSNGNLVAPRGYFKLK  
TKGSSVMRSDAFIDICVSECIIPNGSISNDKPFQNVNKVTVYKCPKIRQNTLKLATG  
MENVPEKQIR"  
30..74  
/gene="HAL"  
75..>1061  
/gene="HAL"  
/product="hemagglutinin"  
ORIGIN  
Query Match 97.6%; Score 1035.4; DB 14; Length 1061;  
Best Local Similarity 98.5%; Pred. No. 1e-235; Indels 0; Gaps 0;  
Matches 1045; Conservative 0; Mismatches 16;  
QY 1 AGCAAAAGCAGGGGATATTTCTGTCATCATGAAGACAACCACTATTTTGATCTACTGA 60  
DB 1 AGCAAAAGCAGGGGATATTTCTGTCATCATGAAGACAACCACTATTTTGATCTACTGA 60  
QY 61 CCATTGGGTCTACAGTCAAAACCCCAACCAAGTGGAAACACAGCCACATTATGTCGG 120  
DB 61 CCATTGGGTCTACAGTCAAAACCCCAACCAAGTGGAAACACAGCCACATTATGTCGG 120  
QY 121 GACACCATGAGTACCAATGGTAAACCAATTAAGTGAACCAATTAAGTGAACCAATTAAGTGA 180  
DB 121 GACACCATGAGTACCAATGGTAAACCAATTAAGTGAACCAATTAAGTGAACCAATTAAGTGA 180  
QY 181 TGACCAATGCTACTGAATTAGTTTTCAGAGCATTTTCAATAGGGAATATGCAACACTCAT 240  
DB 181 TGACCAATGCTACTGAATTAGTTTTCAGAGCATTTTCAATAGGGAATATGCAACACTCAT 240  
QY 241 ATAAAGTCTAGATGAAGAAATTCACATTAATAGATGAATGCTAGAGACCCCACT 300  
DB 241 ATAAAGTCTAGATGAAGAAATTCACATTAATAGATGAATGCTAGAGACCCCACT 300  
QY 301 GTGATCTCTCAGTATGAGAAATGGAGCTCTTTCATAGAGAAAGCAGCGCTTTCAGCA 360  
DB 301 GTGATCTCTCAGTATGAGAAATGGAGCTCTTTCATAGAGAAAGCAGCGCTTTCAGCA 360  
QY 361 ATGTCTACCATATGACATCCCTGACTATGTCATCGCTCCGGTCCATTGTAGCATCTCAG 420  
DB 361 ATGTCTACCATATGACATCCCTGACTATGTCATCGCTCCGGTCCATTGTAGCATCTCAG 420  
QY 421 GAACATTAGAAATTCACAGCAGAGGATTCACATGAGCAGGTGTCTCAAAACCGAAGAA 480  
DB 421 GAACATTAGAAATTCACAGCAGAGGATTCACATGAGCAGGTGTCTCAAAACCGAAGAA 480  
QY 481 GTGAGCGCTCAAAAGGGGATCAGCGGATAGTTTCTTTAGCCGACTGAATGGCTAACAA 540  
DB 481 GTGAGCGCTCAAAAGGGGATCAGCGGATAGTTTCTTTAGCCGACTGAATGGCTAACAA 540  
QY 541 AATCTGGAATCTTACCCCACTGAATGTGCAATGCTCAATCAATAAATAATTCGACA 600  
DB 541 AATCTGGAATCTTACCCCACTGAATGTGCAATGCTCAATCAATAAATAATTCGACA 600  
QY 601 AACTATACATCTGGGGATTCATACCCGAGCTCAACCAACAGCAGCAGCAAGATTGTACA 660  
DB 601 AACTATACATCTGGGGATTCATACCCGAGCTCAACCAACAGCAGCAGCAAGATTGTACA 660  
QY 661 TCCAGAAATCAGGACGAGTAAACAGTCTCAACAAAAAGAGTCAACCAACGATAGTCCCTA 720  
DB 661 TCCAGAAATCAGGACGAGTAAACAGTCTCAACAAAAAGAGTCAACCAACGATAGTCCCTA 720  
QY 721 ATATCGGATCTAGACCGTGGGTAGGGTCAATCAGCAGGATTAAGCATATCTGGACCA 780  
DB 721 ATATCGGATCTAGACCGTGGGTAGGGTCAATCAGCAGGATTAAGCATATCTGGACCA 780  
QY 781 TTGTAAACCTGGAGATATCTTAATGATAACAGTAAATGCACTTATAGTTGCAACCGGG 840  
DB 781 TTGTAAACCTGGAGATATCTTAATGATAACAGTAAATGCACTTATAGTTGCAACCGGG 840

QY 841 GATATTTTAAATTGAAAAACAGGAAAAGCTCTCTAATGAGATCAGATGCAACCCATAGACA 900  
DB 841 GATATTTTAAATTGAAAAACAGGAAAAGCTCTCTAATGAGATCAGATGCAACCCATAGACA 900  
QY 901 TTTGTGTCTCTGAATGTATTACACAAATGGAAGCATCCCCAACGACAAACCATTTTCAA 960  
DB 901 TTTGTGTCTCTGAATGTATTACACCAATGGAAGCATCTCCAAACGACAAACCATTTTCAA 960  
QY 961 ATGTGAACAAAGTTACATATGGAATATGGAATATGGAATATGGAATATGGAATATGGA 1020  
DB 961 ATGTGAACAAAGTTACATATGGAATATGGAATATGGAATATGGAATATGGAATATGGA 1020  
QY 1021 TGGCCACTGGGATGAGGAAATATACCAAGAAAAGCAATCAGA 1061  
DB 1021 TGGCCACTGGGATGAGGAAATATACCAAGAAAAGCAATCAGA 1061  
RESULT 12  
BD244631 1762 bp DNA linear PAT 17-JUL-2003  
LOCUS Low temperature-adaptable equine influenza virus.  
DEFINITION  
ACCESSION BD244631  
VERSION BD244631.1 GI:33054401  
KEYWORDS JP 2002522078-A/7.  
SOURCE Equine influenza virus H3N8  
ORGANISM Viruses; serNA negative-strand viruses; Orthomyxoviridae;  
Influenzavirus A.  
REFERENCE 1 (bases 1 to 1762)  
AUTHORS Dowling, P.W. and Youngner, J.S.  
TITLE Low temperature-adaptable equine influenza virus  
JOURNAL Patent: JP 2002522078-A 7 23-JUL-2002;  
THE UNIVERSITY OF PITTSBURGH OF THE COMMONWEALTH SYSTEM OF HIGHER  
EDUCATION  
COMMENT OS Equine influenza virus H3N8  
PN JP 2002522078-A/7  
PD 23-JUL-2002  
PF 12-AUG-1999 JP 2000565137  
PR 13-AUG-1998 US 09/133921  
PI PATRICIA W DOWLING, JULIUS S YOUNGNER  
PC C12N15/09, A61K39/145, A61P31/16, C07K14/11, C12N7/04, C12N7/04, C12R1:92),  
PC C12N15/00  
CC Low temperature-adaptable equine influenza virus FH Key  
Location/Qualifiers (30)..(1724).  
FT CDS Location/Qualifiers  
source 1..1762  
/organism="Equine influenza virus H3N8"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:31660"  
ORIGIN  
Query Match 97.4%; Score 1033.8; DB 6; Length 1762;  
Best Local Similarity 98.4%; Pred. No. 2.3e-235; Indels 0; Gaps 0;  
Matches 1044; Conservative 0; Mismatches 17;  
QY 1 AGCAAAAGCAGGGGATATTTCTGTCATCATGAAGACAACCACTATTTTGATCTACTGA 60  
DB 1 AGCAAAAGCAGGGGATATTTCTGTCATCATGAAGACAACCACTATTTTGATCTACTGA 60  
QY 61 CCATTGGGTCTACAGTCAAAACCCCAACCAAGTGGCAACCAACAGCCACATTATGTCGG 120  
DB 61 CCATTGGGTCTACAGTCAAAACCCCAACCAAGTGGCAACCAACAGCCACATTATGTCGG 120  
QY 121 GACACCATGAGTACCAATGGTAAACCAATTAAGTGAACCAATTAAGTGAACCAATTAAGTGA 180  
DB 121 GACACCATGAGTACCAATGGTAAACCAATTAAGTGAACCAATTAAGTGAACCAATTAAGTGA 180  
QY 181 TGACCAATGCTACTGAATTAGTTTTCAGAGCATTTTCAATAGGGAATATGCAACACTCAT 240  
DB 181 TGACCAATGCTACTGAATTAGTTTTCAGAGCATTTTCAATAGGGAATATGCAACACTCAT 240

Qy	661	TCCAGAAATCAGGACGAGTAAACAGTCTCAACAAAAAGAACTCAACAAACGATAGTCCTTA	720
Db	661	TCCAGAAATCAGGACGAGTAAACAGTCTCAACAAAAAGAACTCAACAAACGATAGTCCTTA	720
Qy	721	ATATCGGATCTAGACCGTGGGTTTGGGGTCAATCAGCAGGAGTAAGCATATCTGGACCA	780
Db	721	ACATCGGATCTAGACCGTGGGTTTGGGGTCAATCAGCAGGAGTAAGCATATCTGGACCA	780
Qy	781	TTGTAAACCTGGAGATATCCTTAATGATAAACAGTAATGGCAACTTAGTTGCAACCGCGG	840
Db	781	TTGTAAACCTGGAGATATCCTTAATGATAAACAGTAATGGCAACTTAGTTGCAACCGCGG	840
Qy	841	GATATTTTAAATTTGAAACAGGGAAAGCTCTGTATGAGATCAGATGCAACCATAGACA	900
Db	841	GATATTTTAAATTTGAAACAGGGAAAGCTCTGTATGAGATCAGATGCAACCATAGACA	900
Qy	901	TTTGTGTCTGTAATGTATTACACCAATGGAAGCATCCCCAACGACAAACCACTTTCAA	960
Db	901	TTTGTGTCTGTAATGTATTACACCAATGGAAGCATCCCCAACGACAAACCACTTTCAA	960
Qy	961	ATGTGAACAAAGTTACATATGGAATAATGCCCCAAGTATATCAGGCACAAACACATTTAAAGC	1020
Db	961	ATGTGAACAAAGTTACATATGGAATAATGCCCCAAGTATATCAGGCACAAACACATTTAAAGC	1020
Qy	1021	TGGCCACTGGATGAGGATATACCAAGAAAGCAATCAGA	1061
Db	1021	TGGCCACTGGATGAGGATATACCAAGAAAGCAATCAGA	1061

RESULT 11	
AF197242	
LOCUS	
DEFINITION	Influenza A virus (A/equine/Florida/1/94 (H3N8)) linear VRL 08-JAN-2003 precursor (HA1) mRNA, partial cds.
ACCESSION	AF197242
VERSION	AF197242.1
KEYWORDS	GI:6651504
SOURCE	Influenza A virus (A/equine/Florida/1/94 (H3N8))
ORGANISM	Influenza A virus (A/equine/Florida/1/94 (H3N8)) Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenzavirus A.
REFERENCE	1 (bases 1 to 1061)
AUTHORS	Lai, A.C., Chambers, T.M., Holland, R.B. Jr., Morley, P.S., Haines, D.M., Townsend, H.G. and Barrandeguy, M.
TITLE	Diverged evolution of recent equine-2 influenza (H3N8) viruses in the Western Hemisphere
JOURNAL	Arch. Virol. 146 (6), 1063-1074 (2001)
MEDLINE	21395169
PUBMED	11504416
REFERENCE	2 (bases 1 to 1061)
AUTHORS	Lai, A.C.K.
TITLE	Direct Submission
JOURNAL	Submitted (21-OCT-1999) Microbiology & Molecular Genetics, Oklahoma State University, 306 Life Science East, Stillwater, OK 74078, USA
FEATURES	Location/Qualifiers
source	1..1061
	/organism="Influenza A virus
	(A/equine/Florida/1/94 (H3N8))"
	/vion
	/mol_type="mRNA"
	/isolate="A/equine/Florida/1/94"
	/db_xref="taxon:217815"
	/note="H3N8"
	1..1061
	30..>1061
	/gene="HA1"
	/gene="HA1"
	/codon_start=1
	/product="hemagglutinin precursor"
	/protein_id="AAF22346.1"
	/db_xref="GI:6651505"
	/translations="MKTTTIIILLTHWAYSONPTSGNNTATLCIGHHAVANGTLVTKI"
gene	
CDS	

TITLE Identification of two antigenically and genetically distinct lineages of H3N8 equine influenza virus in Sweden

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1100)

AUTHORS Oxburgh, L.H.

TITLE Direct Submission

JOURNAL Submitted (25-JUN-1997) Oxburgh L.H., Veterinary Microbiology, Swedish University of Agricultural Sciences, Biomedical Centre Box 585, s-751 23 Uppsala, SWEDEN

FEATURES

Location/Qualifiers

1..1100

/organism="Influenza A virus (A/equi 2/Soderala/94 (H3N8))"

/virus

/mol\_type="genomic RNA"

/serotype="H3N8"

/isolate="A/equi 2/Soderala/94"

/db\_xref="taxon:217821"

<30..>1100

30..>1100

/codon\_start=1

/product="hemagglutinin HAI subunit"

/protein\_id="CAA74386.1"

/db\_xref="GI:2765370"

/db\_xref="GOA:O56856"

/db\_xref="UniProt/TREMBL:O56856"

/translation="MKTWILLILHCVYSONPIGNNTATLCLGHAVANGTFLVKTITDDQIEVNTATELVQISIGIKCNNSRYVLDGRNCTLIDAMLGDPHCDFQYENWDLFIERSSAFSCPYDIPDYASLSRISVASLGTAEFTWTGVTQNGRSGACKRGSDSPFRLNMLTGSNSYPTLVNTPNNKFNKLYIWIHHPSSNQOETELYIOESGRVTSTFRKQOVTIPNIGSRPWRVSGRISYIWTIVKPGDILMINSNGLVAPRGYFKLVTGKSSVMRSDAPIDICVSECIPTNGSIPNDKPFQNVKVPYKCPKYIQRNTLKLATGMNVPEKQIRGIFGATAGFIENG"

30..1100

/number=1

30..75

ORIGIN

Query Match 97.9%; Score 1039.2; DB 14; Length 1100;

Best Local Similarity 98.8%; Pred. No. 1.3e-236;

Matches 1047; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

2 GCAAAAGCAGGGGATTTCTGTCAATCATGAAGACCAACCATTTTGTATCTAGAC 61

2 GCAAAAGCAGGGGATTTCTGTCAATCATGAAGACCAACCATTTTGTATCTAGAC 61

62 CCATTGGGCTTACAGTCAAAACCAACCAAGTGGAAACACACAGCCACATTATGTCTGG 121

62 CCATTGGTGTACAGTCAAAACCAACCAAGTGGAAACACACAGCCACATTATGTCTGG 121

122 ACACCATGCAGTAGCAATGGAATGGTAAACCAATCAATCAATCAATCAATCAATCAAT 181

122 ACACCATGCAGTAGCAATGGAATGGTAAACCAATCAATCAATCAATCAATCAATCAAT 181

182 GACAAATGCTACTGAATTTAGTTCAGAGCATTTCAATAGGGAAATATGCAACCACTCATA 241

182 GACAAATGCTACTGAATTTAGTTCAGAGCATTTCAATAGGGAAATATGCAACCACTCATA 241

242 TAAAGTTCTAGTGAAGAAATTTGCACATTAATAGATGCAATGCTAGGACACCCCACTG 301

242 TAGAGTTCTAGTGAAGAAATTTGCACATTAATAGATGCAATGCTAGGACACCCCACTG 301

302 TGATGCTCTCCAGTATGAGAAATTTGGGACCTTTCATAGAAAGAGCAGCGCTTTCAGCAA 361

302 TGATGCTCTCCAGTATGAGAAATTTGGGACCTTTCATAGAAAGAGCAGCGCTTTCAGCAA 361

362 TTGCTACCCATATGACATCCCTGACTATGATGCTCCCGTCCATTGTAGCATCTCTCAGG 421

362 TTGCTACCCATATGACATCCCTGACTATGATGCTCCCGTCCATTGTAGCATCTCTCAGG 421

422 AACATTAGAATTCACACAGAGGATTCACATGACAGGTTCTCACTCAAAACCGAGAGAG 481

422 AACATTGGAATTCACACAGAGGATTCACATGACAGGTTCTCACTCAAAACCGAGAGAG 481

482 TGGAGCCTGCAAAAGGGGATCAGCGATAGTTTCTTTAGCCGACTGAATTTGGCTAACAAA 541

482 TGGAGCCTGCAAAAGGGGATCAGCGATAGTTTCTTTAGCCGACTGAATTTGGCTAACAAA 541

542 ATCTGGAATCTTTRACCCACATTTGAATGTGACATGCTTAACATAAATAATTTTCGACAA 601

542 ATCTGGAATCTTTRACCCACATTTGAATGTGACATGCTTAACATAAATAATTTTCGACAA 601

602 ACTATACATCTGGGGGATTTCACTCCCGAGCTCAAAACCAACAGCAGACAGAAATTTGACAT 661

602 ACTATACATCTGGGGGATTTCACTCCCGAGCTCAAAACCAACAGCAGACAGAAATTTGACAT 661

662 CCAAGAAATCAGCAGCAGTAACAGTCTCAACAAAAAGAGTCAACAAACGATAGTCCCTAA 721

662 CCAAGAAATCAGCAGCAGTAACAGTCTCAACAAAAAGAGTCAACAAACGATAGTCCCTAA 721

722 TATCGGATCTAGACCGTGGGTTAGGGGTCAATCAGGAGGATAAGCATATATCTGGACCAT 781

722 TATCGGATCTAGACCGTGGGTTAGGGGTCAATCAGGAGGATAAGCATATATCTGGACCAT 781

782 TGTAAACCTGAGATATCTTAATGATAAACAGATTAATGGCAACTTAGTTGCACCGGGGG 841

782 TGTAAACCTGAGATATCTTAATGATAAACAGATTAATGGCAACTTAGTTGCACCGGGGG 841

842 ATATTTTAAATTTGAAAACAGGGGAAAGCTCTGTAAATGAGATCAGATGCACCCATGACAT 901

842 ATATTTTAAATTTGAAAACAGGGGAAAGCTCTGTAAATGAGATCAGATGCACCCATGACAT 901

902 TTGTGTCTGTAATGTTATACCAAAATGGAAGCATCTCCCAACGACCAACCATTTTCAAA 961

902 TTGTGTCTGTAATGTTATACCAAAATGGAAGCATCTCCCAACGACCAACCATTTTCAAA 961

962 TGTGAACAAAGTTACATATGGAATAATGCCCAAGTATATCAGGCAAAACACCTTTAAAGCT 1021

962 TGTGAACAAAGTTACATATGGAATAATGCCCAAGTATATCAGGCAAAACACCTTTAAAGCT 1021

1022 GGCCACTGGGATGAGGAATATACCAAGAAAGCAAAATCAGA 1061

1022 GGCCACTGGGATGAGGAATATACCAAGAAAGCAAAATCAGA 1061

RESULT 10

FLAH3F

LOCUS Influenza A/Equine/Kentucky/1/91 hemagglutinin (HAI) gene, complete cds.

DEFINITION

FLAH3F 1762 bp ss-RNA linear VRL 29-NOV-1996

INFLUENZA A/EQUINE/KENTUCKY/1/91

ACCESSION L39918

VERSION L39918.1

GI:722411

SOURCE

INFLUENZA A VIRUS (STRAIN A/EQUINE/KENTUCKY/1/91)

INFLUENZA A VIRUS (STRAIN A/EQUINE/KENTUCKY/1/91)

ORGANISM

Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;

INFLUENZAVIRUS A.

REFERENCE 1 (bases 1 to 1762)

AUTHORS Dally, J.M., Lai, A.C., Binns, M.M., Chambers, T.M., Barrandeguy, M. and Mumford, J.A.

TITLE Antigenic and genetic evolution of equine H3N8 influenza A viruses

JOURNAL J. Gen. Virol. 77 (Pt 4), 661-671 (1996)

MEDLINE 96203953

PUBMED 8627254

FEATURES

Location/Qualifiers

1..1762

/organism="Influenza A virus (strain A/equine/Kentucky/1/91)"

/mol\_type="genomic RNA"

/strain="Equine-2"

/isolate="A/Equine/Kentucky/1/91"

/db\_xref="taxon:38828"

/clone="2554"

30..1727

/gene="HA1"

30..1727

/gene="HA1"

gene

CDS

```

DEFINITION Influenza A/Equine/Florida/1/93 hemagglutinin (HA1) gene, complete
            cds.
ACCESSION L39916
VERSION L39916.1 GI:722407
KEYWORDS
SOURCE Influenza A virus (strain A/equine/Florida/1/93)
ORGANISM Influenza A virus (strain A/equine/Florida/1/93)
          Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
          Influenzavirus A.
REFERENCE 1 (bases 1 to 1762)
AUTHORS Daly,J.M., Lai,A.C., Binns,M.M., Chambers,T.M., Barrandeguy,M. and
          Mumford,J.A.
TITLE Antigenic and genetic evolution of equine H3N8 influenza A viruses
JOURNAL J. Gen. Virol. 77 (Pt 4), 661-671 (1996)
MEDLINE 96203953
PUBMED 8627254
FEATURES
    Location/Qualifiers
        1..1762
            /organism="Influenza A virus (strain
            A/equine/Florida/1/93)"
            /mol_type="genomic RNA"
            /strain="Equine-2"
            /isolate="A/Equine/Florida/1/93"
            /db_xref="taxon:39124"
            /clone="2763"
            30..1727
                /gene="HA1"
            30..1727
                /gene="HA1"
            /codon_start=1
            /product="hemagglutinin"
            /protein_id="AAB36978.1"
            /db_xref="GI:722408"
            /translation="MKTIIILITLHWVSNPTSGNNTATILCLGHAVANGTLVKTI
            TDDQEVNATLVSISIGKICNNSYRVLGRNCTLIDMLGDPHCDVQYEWDLF
            IERSAFNCYPIDIPDVLASLSIVASSGTLEFAGFTWGTQNGSRGACKRGS
            SPFSLNLWLTSGNSYPLTNPNKNPDKLYIWIHHPSSNQTKLYIQSGSRVT
            VTKRSQOTIIPNIGSRPWRQSGRIISYIWTIVKPGDILMINSNGNIVAPRGYFKL
            TGKSWMSDAPIDICVSECIIPNGISNDKPFQNVKVTYQKPKYRONTLKLAT
            MNVPEKOIRGIFGAIAQFIENGWGVWGYPRYQNSEGTGAADI.KSTCAADQI
            NGKLNVERTNEKHEQIEKSEFVEGRIQDLEKYVETKIDLSYNALIELVALENQH
            TIDLDAENMKLEFKTRQLENADMGCGCPKIYHKCDNACIGSIRNGTVDHYIYRD
            EALNNRFOIKGVELKSGYKDWLTWISFTISCFILICVLLGFTIMWACQGNIRCNICI"
            30..74
                /gene="HA1"
                /note="putative"
            75..1724
                /gene="HA1"
            /product="hemagglutinin"
            /note="includes HA1 and HA2"
            75..1061
                /gene="HA1"
            /product="hemagglutinin"
sig_peptide
mat_peptide
mat_peptide
mat_peptide
ORIGIN
Query Match 98.2%; Score 1041.8; DB 14; Length 1762;
Best Local Similarity 98.9%; Pred. No. 2.9e-237;
Matches 1049; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1 AGCAAAAGCAGGGGATATTTCTGTCATCATGACGACACCACTATTATTTGATCTACTGA 60
DB 1 AGCAAAAGCAGGGGATATTTCTGTCATCATGACGACACCACTATTATTTGATCTACTGA 60
QY 61 CCATTGGGTCTACAGTCAAAACCCCAACCCAGTGGAAACCAACACAGCCACATTATGCTGG 120
DB 61 CCATTGGGTCTACAGTCAAAACCCCAACCCAGTGGAAACCAACACAGCCACATTATGCTGG 120
QY 121 GACACCATGACATAGCAATGGAAACATTTGGTAAACCAATAACTGATGACCAAAATTTGAGG 180
DB 121 GACACCATGACATAGCAATGGAAACATTTGGTAAACCAATAACTGATGACCAAAATTTGAGG 180
QY 181 TGACAAATGCTACTGAATTTAGTTCAGAGCATTTCAATAGGAAAAATATGCAACAACTCAT 240

```

```

DB 181 TGACAAATGCTACTGAATTTAGTTCAGAGCATTTCAATAGGAAAAATATGCAACAACTCAT 240
QY 241 ATAAAGTTCTAGATGGAAGAAATTCGACATTAATAGATGCAATGCTAGGAGACCCCACT 300
DB 241 ATAGAGTTCTAGATGGAAGAAATTCGACATTAATAGATGCAATGCTAGGAGACCCCACT 300
QY 301 GTGATGCTTCCAGTATGAGAATTTGGGACCTCTTTCATAGAAGAACGACGCGTTTCAGCA 360
DB 301 GTGATGCTTCCAGTATGAGAATTTGGGACCTCTTTCATAGAAGAACGACGCGTTTCAGCA 360
QY 361 ATTGCTACCATATGACATCCCTGACATGATGCTCGGTCCGATGCTAGGATCTTCAAG 420
DB 361 ATTGCTACCATATGACATCCCTGACATGATGCTCGGTCCGATGCTAGGATCTTCAAG 420
QY 421 GAACATTAAGAAATTCACAGCAGAGGATTCATATGACAGAGGTGTCACTCAAAAACGGAAGA 480
DB 421 GAACATTAAGAAATTCACAGCAGAGGATTCATATGACAGAGGTGTCACTCAAAAACGGAAGA 480
QY 481 GTGAGCGCTGCAAAAGGGGATCAGCCGATAGTTCTTTAGCGGACTGAATTTGGCTTAA 540
DB 481 GTGAGCGCTGCAAAAGGGGATCAGCCGATAGTTCTTTAGCGGACTGAATTTGGCTTAA 540
QY 541 AATCTGGAACCTCTTACCCGACATTTGAATGTGACATGCTTAAATTAATAATTTTCGACA 600
DB 541 AATCTGGAACCTCTTACCCGACATTTGAATGTGACATGCTTAAATTAATAATTTTCGACA 600
QY 601 AACTATACATCTGGGGGATTCATACCCGAGTCAAAACCAACAGCAGACAGAAATTTGACA 660
DB 601 AACTATACATCTGGGGGATTCATACCCGAGTCAAAACCAACAGCAGACAGAAATTTGACA 660
QY 661 TCCAAGAAATCAGGACGAGTAAACAGTCTCAACAAAAAGAAAGTCAACAAACAAATAATCCCTA 720
DB 661 TCCAAGAAATCAGGACGAGTAAACAGTCTCAACAAAAAGAAAGTCAACAAACAAATAATCCCTA 720
QY 721 ATATCGGATCTAGACCGTGGGTAGGCGTCAATCAGGCGAGGATAGCATATATCTGACCA 780
DB 721 ACATCGGATCTAGACCGTGGGTAGGCGTCAATCAGGCGAGGATAGCATATATCTGACCA 780
QY 781 TTGTAAAACCTGGAGATATCTTAATGATAACAGTAAATGGCAACTTAGTTGACCGCGGG 840
DB 781 TTGTAAAACCTGGAGATATCTTAATGATAACAGTAAATGGCAACTTAGTTGACCGCGGG 840
QY 841 GATATTTTAAATGAAAAACAGGAAAAGCTCTGTAATGAGATCAGATGACCCCATAGACA 900
DB 841 GATATTTTAAATGAAAAACAGGAAAAGCTCTGTAATGAGATCAGATGACCCCATAGACA 900
QY 901 TTTGTGTCCTGAATGTAATACCAATGAGAGTCCCAACGACGACAAACCAATTTTCAA 960
DB 901 TTTGTGTCCTGAATGTAATACCAATGAGAGTCCCAACGACGACAAACCAATTTTCAA 960
QY 961 ATGTGAACAAAGTTACATATGGAATAATGCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
DB 961 ATGTGAACAAAGTTACATATGGAATAATGCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
QY 1021 TGGCCACTGGGATGAGGAATATACAGAAAAAGCAAAATCAGA 1061
DB 1021 TGGCCACTGGGATGAGGAATATACAGAAAAAGCAAAATCAGA 1061
RESULT 9
EIVY14058 1100 bp RNA linear VRL 11-JAN-2003
LOCUS Influenza A virus (A/equi 2/Soderala/94(H3N8)) gene for
DEFINITION hemagglutinin HA1 subunit, isolate A/equi 2/Soderala/94.
ACCESSION Y14058
VERSION Y14058.1 GI:2765369
KEYWORDS hemagglutinin HA1 subunit.
SOURCE Influenza A virus (A/equi 2/Soderala/94(H3N8))
ORGANISM Influenza A virus (A/equi 2/Soderala/94(H3N8))
          Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
          Influenzavirus A.
REFERENCE 1 (bases 1 to 1100)
AUTHORS Oxburgh,L., Akertblom,L., Fridberger,T., Klingeborn,B. and Linne,T.

```

Db 841 AAATTGAAACAGGGAAGCTCTGTATAGATCAGATGACGACCCATACACATTTGTGG 900  
QY 909 TCTGAATGATTATACCAATATGAAGCATCCCAAGCAAAACCATTTCAAATGTGAAC 968  
Db 901 TCTGAATGATTATACCAATATGAAGCATCCCAAGCAAAACCATTTCAAATGTGAAC 960  
QY 969 AAAGTTTACATATGGAATATGCCCCCAAGTATATCAGGCAAAACCATTTTAAAGCTGGCCACT 1028  
Db 961 AAAGTTTACATATGGAATATGCCCCCAAGTATATCAGGCAAAACCATTTTAAAGCTGGCCACT 1020  
QY 1029 GGGATGAGGAATATACCAAGAAAGCAAAATCAGA 1061  
Db 1021 GGGATGAGGAATGCTACCAAGAAAGCAAAATCAGA 1053

## RESULT 7

EIVY14060  
LOCUS  
DEFINITION  
Influenza A virus (A/equi 2/Bollnas/96(H3N8)) gene for  
hemagglutinin HAI subunit, isolate A/equi 2/Bollnas/96.  
Y14060  
ACCESSION  
VERSION  
Y14060.1 GI:2765373  
KEYWORDS  
SOURCE  
Influenza A virus (A/equi 2/Bollnas/96(H3N8))  
ORGANISM  
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
Influenzavirus A.

REFERENCE  
AUTHORS  
Oxburgh, L., Akerblom, L., Fridberger, T., Klingeborn, B. and Linne, T.  
TITLE  
Identification of two antigenically and genetically distinct  
lineages of H3N8 equine influenza virus in Sweden  
JOURNAL  
Unpublished  
REFERENCE  
AUTHORS  
Oxburgh, L.H.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (25-JUN-1997) Oxburgh L.H., Veterinary Microbiology,  
Swedish University of Agricultural Sciences, Biomedical Centre Box  
585, s-751 23 Uppsala, SWEDEN

## FEATURES

source  
1. .1060  
/organism="Influenza A virus (A/equi 2/Bollnas/96(H3N8))"  
/virus  
/mol\_type="genomic RNA"  
/serotype="H3N8"  
/isolate="A/equi 2/Bollnas/96"  
/db\_xref="taxon:217819"  
<22..1060  
22..>1060  
/codon\_start=1  
/product="hemagglutinin HAI subunit"  
/protein\_id="CA74388.1"  
/db\_xref="GI:2765374"  
/db\_xref="GOA:O56858"  
/db\_xref="UniProt/TREMBL:O56858"  
/translation="MKTTILILLTHWVSQNPSTGNNTATILGHHAHVANGTLVKTI  
TNDQIVTATLQVSIIGKLCNNYSRVLDGNCTLIDAMLGDPDCHDFVQYENMDLF  
IERSSAFSNCYPIDIDYASLSISIVASSGTLPTAGFTWTGWTONGRSGACKRSAD  
SFSRLNWLTKSGNSIPTLVNTPNNKFNFKLGIWIHPSPNQOITELITQESRVT  
VTSKRSQQTIIINIGSRPVRVQSGRSISYTWIVKPDILMINSGNLVAPRGYFKLK  
TKSSVYMRSDAPTDIICASECITPNSIPNDKFPQNVKVTYKCPKYIRONTLKLATG  
MRNVEKQIRGI"  
22..1060  
/number=1  
22.. .67

## sig\_peptide

## ORIGIN

Query Match 98.2%; Score 1041.8; DB 14; Length 1060;  
Best Local Similarity - 99.3%; Pred. No. 31e-237;  
Matches 1046; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 9 CAGGGGATATTTCTGCAATCATGAAGCAACCATTTATTTGTACTACTGACCCCATTTGG 68  
Db 1 CAGGGGATATTTCTGCAATCATGAAGCAACCATTTATTTGTACTACTGACCCCATTTGG 60

QY 69 GTCTACAGTCAAAACCCCAACAGTGGAAACCAACAGCACCAATTATGTCTGGGACACCAT 128  
Db 61 GTCTACAGTCAAAACCCCAACAGTGGAAACCAACAGCACCAATTATGTCTGGGACACCAT 120  
QY 129 GCAGTAGCAAAATGGAAACATTTGGTAAAAACAATAAATCTAGTAGCAAAATTTGAGGTGA 188  
Db 121 GCAGTAGCAAAATGGAAACATTTGGTAAAAACAATAAATCTAGTAGCAAAATTTGAGGTGA 180  
QY 189 GCTACTGAATTTAGTTTCAGAGCATTTCAATAGGGAAAAATATGCAACCACTCATATAAGTT 248  
Db 181 GCTACTGAATTTAGTTTCAGAGCATTTCAATAGGGAAAAATATGCAACCACTCATATAAGTT 240  
QY 249 CTAGATGGAAGAAATTTGCACATTAATAGATCAATGCTAGGAGAGCCCCCACTGTGATGC 308  
Db 241 CTAGATGGAAGAAATTTGCACATTAATAGATCAATGCTAGGAGAGCCCCCACTGTGATGC 300  
QY 309 TTCCAGTATGAGAAATTTGGACCTCTTCATAGAAAGACGAGCGCTTTTCAGCAATGCTAC 368  
Db 301 TTCCAGTATGAGAAATTTGGACCTCTTCATAGAAAGACGAGCGCTTTTCAGCAATGCTAC 360  
QY 369 CCATATGACATCCCTGACATATGATCGCTCCGCTCCATTTAGCATCTCTCAGGAACATTA 428  
Db 361 CCATATGACATCCCTGACATATGATCGCTCCGCTCCATTTAGCATCTCTCAGGAACATTA 420  
QY 429 GAATTTACAGCAGAGGGGATTCACATGGACAGGTGTCTCAAAAACGGAAGAGTGGAGCC 488  
Db 421 GAATTTACAGCAGAGGGGATTCACATGGACAGGTGTCTCAAAAACGGAAGAGTGGAGCC 480  
QY 489 TGCAAAAGGGGATCAGCCGATAGTTCTTTTAGCCGACGTAAGTGGCTTACAAAATCTGA 548  
Db 481 TGCAAAAGGGGATCAGCCGATAGTTCTTTTAGCCGACGTAAGTGGCTTACAAAATCTGA 540  
QY 549 AACTCTTACCCACATTTGAATGTGCAATGCTTACCAATTAATAATTTTCGACAACTATAC 608  
Db 541 AACTCTTACCCACATTTGAATGTGCAATGCTTACCAATTAATAATTTTCGACAACTATAC 600  
QY 609 ATCTCGGGGATTCATCACCCGAGCTCAAAACCAACAGCAGACAGAAATTTGACATCCAAGAA 668  
Db 601 ATCTCGGGGATTCATCACCCGAGCTCAAAACCAACAGCAGACAGAAATTTGACATCCAAGAA 660  
QY 669 TCAGGACGAGTAACTCTCAACAAAAGAGTCAACAAACGATAGTCCCTTAATATCGGA 728  
Db 661 TCAGGACGAGTAACTCTCAACAAAAGAGTCAACAAACGATAGTCCCTTAATATCGGA 720  
QY 729 TCTAGACCGTGGTTAGGGGTCAATCAGCAGGATTAAGCATATCTGGACCATTTGTAAA 788  
Db 721 TCTAGACCGTGGTTAGGGGTCAATCAGCAGGATTAAGCATATCTGGACCATTTGTAAA 780  
QY 789 CCTGAGGATATCTTAATGATAACAGTAATGGCAACTTAGTTGCAACCGGGGATATTTT 848  
Db 781 CCTGAGGATATCTTAATGATAACAGTAATGGCAACTTAGTTGCAACCGGGGATATTTT 840  
QY 849 AAATGAAAACAGGGAAGTCTCTGTATAGATCAGATGCAACCAATAGACATTTGTGTG 908  
Db 841 AAATGAAAACAGGGAAGTCTCTGTATAGATCAGATGCAACCAATAGACATTTGTGTG 900  
QY 909 TCTGATGTTATTACCAAAATGGAAGCATCCCAACGACAAACCATTTTCAAATGTGAAC 968  
Db 901 TCTGATGTTATTACCAAAATGGAAGCATCCCAACGACAAACCATTTTCAAATGTGAAC 960  
QY 969 AAAGTTTACATATGGAATATGCCCCCAAGTATATCAGGCAAAACCATTTTAAAGCTGGCCACT 1028  
Db 961 AAAGTTTACATATGGAATATGCCCCCAAGTATATCAGGCAAAACCATTTTAAAGCTGGCCACT 1020  
QY 1029 GGGATGAGGAATATACCAAGAAAGCAAAATCAGA 1061  
Db 1021 GGGATGAGGAATATACCAAGAAAGCAAAATCAGA 1053

## RESULT 8

FLAH3D  
LOCUS

FLAH3D 1762 bp ss-RNA linear VRL 29-NOV-1996

```
QY 601 AACTATACATCTGGGGGATTCATACCCGAGCTCAAAACCAACAGCAGACAGAAATGTACA 660
Db 601 AACTATACATCTGGGGGATTCATACCCGAGCTCAAAACCAACAGCAGAAATGTACA 660
QY 661 TCCAAGAAATCAGGACGAGTAACAGTCTCAACAAAAAGAAAGTCAACAAACGATAATCCCTA 720
Db 661 TCCAAGAAATCAGGACGAGTAACAGTCTCAACAAAAAGAAAGTCAACAAACGATAATCCCTA 720
QY 721 ATATCGGATCTAGACCGTGGGTAGGGTCAATCAGGAGGATAAGCATATATCTGACCA 780
Db 721 ATATCGGATCTAGACCGTGGGTAGGGTCAATCAGGAGGATAAGCATATATCTGACCA 780
QY 781 TTATAAACCTCGAGATATCTTAATGATATAACAGTAATGGCAACTTAGTTGCACCGCGGG 840
Db 781 TTATAAACCTCGAGATATCTTAATGATATAACAGTAATGGCAACTTAGTTGCACCGCGGG 840
QY 841 GATATTTTAAATGAAAAACAGGGAAGCTCTGTATGAGATCAGATGCACCCATAGACA 900
Db 841 GATATTTTAAATGAAAAACAGGGAAGCTCTGTATGAGATCAGATGCACCCATAGACA 900
QY 901 TTTGTGTGCTCAATCTATTACCAAAATGGAGGATCCCAACGACAAACCATTTCAA 960
Db 901 TTTGTGTGCTCAATCTATTACCAAAATGGAGGATCCCAACGACAAACCATTTCAA 960
QY 961 ATGTGAACAAAGTTACATATGGAATGCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
Db 961 ATGTGAACAAAGTTACATATGGAATGCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
QY 1021 TGGCCACTGGGATGAGGAATATACCGAAAAAGCAATCAGA 1061
Db 1021 TGGCCACTGGGATGAGGAATATACCGAAAAAGCAATCAGA 1061
```

## RESULT 6

```
EIVY14059
LOCUS      1060 bp      RNA      linear      VRL 11-JAN-2003
DEFINITION Influenza A virus (A/equi 2/Alvdalen/96(H3N8)) gene for
            hemagglutinin HA1 subunit, isolate A/equi 2/Alvdalen/96.
ACCESSION Y14059
VERSION    Y14059.1 GI:2765371
KEYWORDS   hemagglutinin HA1 subunit.
SOURCE     Influenza A virus (A/equi 2/Alvdalen/96(H3N8))
ORGANISM   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE  1 (bases 1 to 1060)
AUTHORS    Oxburgh, L., Akerblom, L., Fridberger, T., Klingeborn, B. and Linne, T.
TITLE      Identification of two antigenically and genetically distinct
            lineages of H3N8 equine influenza virus in Sweden
JOURNAL    Unpublished
AUTHORS    Oxburgh, L.H.
TITLE      Direct Submission
JOURNAL    Submitted (25-JUN-1997) Oxburgh L.H., Veterinary Microbiology,
            Swedish University of Agricultural Sciences, Biomedical Centre Box
            585, s-751 23 Uppsala, SWEDEN
FEATURES   Location/Qualifiers
            1..1060
             /organism="Influenza A virus (A/equi 2/Alvdalen/96(H3N8))"
             /viral
             /mol_type="genomic RNA"
             /serotype="H3N8"
             /isolate="A/equi 2/Alvdalen/96"
             /db_xref="taxon:217820"
             <22..>1060
             22..>1060
             /codon_start=1
             /product="hemagglutinin HA1 subunit"
             /protein_id="CAA74387.1"
             /db_xref="GI:2765372"
             /db_xref="GOA:O56857"
             /db_xref="UniProt/TREMBL:O56857"
             /translation="MKTTILILLTHWVYQNPTSGNNTATILCLGHAVANGTLVTKTI
```

mRNA  
CDS

```

TNDQLEVTNATVQSISIGKICNNISYRVLDGRNCTLIDAMLDPDCHDVFQYOVNWLFI
IERSSAFNCPYDIPDYASLRISIVASGTLFTAEAGTGTGVTONGSGAGCKRSAD
SPFSLRWLTKSGNSYPTLANTYPMNNKPFKLYIWGJHPSNQQOQTLTJQESRVT
VSTRSQOITIIPIGSRPWQGRISIIYWTIVKPGDILMINSNGLVAPRGYFKLK
TGSVMRSMDAPIDICASECITPNGISIPDKFQNVNKVTYKCPKIRQNTLKLATG
NRNYPEKQIRGI"
22..1060
/number=1
sig_peptide 22..67
ORIGIN
Query Match 98.3%; Score 1043.4; DB 14; Length 1060;
Best Local Similarity 99.4%; Pred. No. 1.3e-237;
Matches 1047; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 9 CAGGGGATATTTCTGTCATCATGAGACACCAATATTTTGATACTACTGACCCATTGG 68
Db 1 CAGGGGATATTTCTGTCATCATGAGACACCAATATTTTGATACTACTGACCCATTGG 60
QY 69 GTCTACAGTCAAAACCCCAACAGTCGGAACACACAGCCACATTTATGTCTGGGACACCAT 128
Db 61 GTCTACAGTCAAAACCCCAACAGTCGGAACACACAGCCACATTTATGTCTGGGACACCAT 120
QY 129 GCAGTAGCAAAATGGAAACATTTGGTAAAAACAATACTGATGACCAAAATTTGAGGTGCAAAAT 188
Db 121 GCAGTAGCAAAATGGAAACATTTGGTAAAAACAATACTGATGACCAAAATTTGAGGTGCAAAAT 180
QY 189 GCTACTGAATTTAGTTTCAGAGCATTTCAATAGGGAATATGCAACCACTCATATAAGTT 248
Db 181 GCTACTGAATTTAGTTTCAGAGCATTTCAATAGGGAATATGCAACCACTCATATAAGTT 240
QY 249 CTAGATGAAGAAATTTGACATTAATAGATGCAATGCTAGGAGAGCCGCCACTGTGATGTC 308
Db 241 CTAGATGAAGAAATTTGACATTAATAGATGCAATGCTAGGAGAGCCGCCACTGTGATGTC 300
QY 309 TTCCAGTATGAGAAATTTGGGACCTCTTCTATAGAAAGACAGCGCTTTTTCAGCAATTTGCTAC 368
Db 301 TTCCAGTATGAGAAATTTGGGACCTCTTCTATAGAAAGACAGCGCTTTTTCAGCAATTTGCTAC 360
QY 369 CCATATGATATCCCTGACTATGCTATGCTCGGTCCATTTAGTATGCTCTCAGGACATTA 428
Db 361 CCATATGATATCCCTGACTATGCTATGCTCGGTCCATTTAGTATGCTCTCAGGAAACATTTG 420
QY 429 GAAATTCAGCAGAGGGGATTCACATGGACAGGTGTCTCTCAAAACGGAAGAGTGGAGCC 488
Db 421 GAAATTCAGCAGAGGGGATTCACATGGACAGGTGTCTCTCAAAACGGAAGAGTGGAGCC 480
QY 489 TGCAAAAGGGGATTCAGCCGATAGTTTCTTTAGCCGACTGAAATTTGGCTAAACAAATCTGGA 548
Db 481 TGCAAAAGGGGATTCAGCCGATAGTTTCTTTAGCCGACTGAAATTTGGCTAAACAAATCTGGA 540
QY 549 AACTCTTACCCACATTTGAATGTGCAATGCTTAACATTAATAATTTTCGACAACTATAC 608
Db 541 AACTCTTACCCACATTTGAATGTGCAATGCTTAACATTAATAATTTTCGACAACTATAC 600
QY 609 ATCTGGGGGATTCATCACCGAGCTCAAAACCAACAGCAGACAGAAATTTGTACATCAAGAA 668
Db 601 ATCTGGGGGATTCATCACCGAGCTCAAAACCAACAGCAGACAGAAATTTGTACATCAAGAA 660
QY 669 TCAGGACGAGTAACAGTCTCAACAAAAAGAAAGTCAACAAACGATAGTCCCTAATATCGGA 728
Db 661 TCAGGACGAGTAACAGTCTCAACAAAAAGAAAGTCAACAAACGATAGTCCCTAATATCGGA 720
QY 729 TCTAGACCGTGGGTTAGGGGTCAATCAGGAGGATAAGCATATCTGAGCCATTTCTAAA 788
Db 721 TCTAGACCGTGGGTTAGGGGTCAATCAGGAGGATAAGCATATCTGAGCCATTTGTAAA 780
QY 789 CTGGAGATATCTCTAATGATAAAACAGTAATGCAACTTAGTTGACCGCGGGATATTTT 848
Db 781 CTGGAGATATCTCTAATGATAAAACAGTAATGCAACTTAGTTGACCGCGGGATATTTT 840
QY 849 AAATTTGAAAAACAGGGGAAAGCTCTCTAATGAGATCAGATGCAACCCATAGACATTTGTGTG 908
Db 849 AAATTTGAAAAACAGGGGAAAGCTCTCTAATGAGATCAGATGCAACCCATAGACATTTGTGTG 908
```



```
QY 241 ATAAAGTCTTAGATGAAGAAATTCACATTAATAGATCAATGTAGGAGACCCCACT 300
Db 241 ATAGAGTCTTAGATGAAGAAATTCACATTAATAGATCAATGTAGGAGACCCCACT 300
QY 301 GTGATGCTTCCAGTATGAGAAATGGACCTTTCATAGAAAGAGCAGCGCTTTCAGA 360
Db 301 GTGATGCTTCCAGTATGAGAAATGGACCTTTCATAGAAAGAGCAGCGCTTTCAGA 360
QY 361 ATGCTACCCCATATGACATCCCTGACTATGATCGCTCGGTCCATTTGAGCATCTCAG 420
Db 361 ATGCTACCCCATATGACATCCCTGACTATGATCGCTCGGTCCATTTGAGCATCTCAG 420
QY 421 GAACATTAAGAAATTCACAGCAGAGGATTCACATGACAGAGGTCTCACTCAAAACGGAAGA 480
Db 421 GAACATTAAGAAATTCACAGCAGAGGATTCACATGACAGAGGTCTCACTCAAAACGGAAGA 480
QY 481 GTGAGCTGCAAAAGGGGATCAGCGGATAGTTTCTTACCGGACTGAATTTGGCTTAACA 540
Db 481 GTGAGCTGCAAAAGGGGATCAGCGGATAGTTTCTTACCGGACTGAATTTGGCTTAACA 540
QY 541 AATCTGGAACCTCTTACCCCATATGAAATGTGACAAATGCTCAACAAATTAATAATTCGACA 600
Db 541 AATCTGGAACCTCTTACCCCATATGAAATGTGACAAATGCTCAACAAATTAATAATTCGACA 600
QY 601 AACTATACATCTGGGGGATTCATACCCGAGCTCAAAACCAACAGCAGACAGAAATTTGACA 660
Db 601 AACTATACATCTGGGGGATTCATACCCGAGCTCAAAACCAACAGCAGACAGAAATTTGACA 660
QY 661 TCAAGATCAGGACAGTAAAGTCTCAAAAGAAAGTCAAAAGCAGATAGTCCCTA 720
Db 661 TCAAGATCAGGACAGTAAAGTCTCAAAAGAAAGTCAAAAGCAGATAGTCCCTA 720
QY 721 ATATCGGATCTAGACCTGGGTAGGGTCAATCAGGAGGATAGGATATATCTGACCA 780
Db 721 ATATCGGATCTAGACCTGGGTAGGGTCAATCAGGAGGATAGGATATATCTGACCA 780
QY 781 TTGTAACCTGGAGATATCTTAATGATAAAACAGTAATGGCACTTAGTTGACCGCGGG 840
Db 781 TTGTAACCTGGAGATATCTTAATGATAAAACAGTAATGGCACTTAGTTGACCGCGGG 840
QY 841 GATATTTTAAATGAAACAGGAAAGCTCTGTAATGAGATCAGATGACCCCATAGACA 900
Db 841 GATATTTTAAATGAAACAGGAAAGCTCTGTAATGAGATCAGATGACCCCATAGACA 900
QY 901 TTGTTGTCTGAATGTTATACCAAAATGGAAGCATCCCAACGACAAACCATTTCAAA 960
Db 901 TTGTTGTCTGAATGTTATACCAAAATGGAAGCATCCCAACGACAAACCATTTCAAA 960
QY 961 ATGTGAACAAAGTTACATATGAAATGCCCAAGTATATATCAGGCAAAACACTTTAAAGC 1020
Db 961 ATGTGAACAAAGTTACATATGAAATGCCCAAGTATATATCAGGCAAAACACTTTAAAGC 1020
QY 1021 TGGCCACTGGGATGAGGATATACAGAAAGCAATTCGA 1061
Db 1021 TGGCCACTGGGATGAGGATATACAGAAAGCAATTCGA 1061
```

```
RESULT 4
AF197247
LOCUS AF197247 1061 bp mRNA linear VRL 08-JAN-2003
DEFINITION Influenza A virus (A/equine/Kentucky/9/95 (H3N8)) hemagglutinin precursor (HA1) mRNA, partial cds.
ACCESSION AF197247
VERSION AF197247.1 GI:6651514
KEYWORDS Influenza A virus (A/equine/Kentucky/9/95 (H3N8))
SOURCE Influenza A virus (A/equine/Kentucky/9/95 (H3N8))
ORGANISM Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenzavirus A.
REFERENCE 1 (bases 1 to 1061)
AUTHORS Lai,A.C., Chambers,T.M., Holland,R.E. Jr., Morley,P.S., Haines,D.M., Townsend,H.G. and Barrandeguy,M.
TITLE Diverged evolution of recent equine-2 influenza (H3N8) viruses in
```

```
JOURNAL the Western Hemisphere
MEDLINE Arch. Virol. 146 (6), 1063-1074 (2001.)
PUBMED 21395169
REFERENCE 2 (bases 1 to 1061)
AUTHORS Lai,A.C.K.
TITLE Direct Submission
JOURNAL Submitted (21-OCT-1999) Microbiology & Molecular Genetics, Oklahoma State University, 306 Life Science East, Stillwater, OK 74078, USA
FEATURES
source
1..1061
/organism="Influenza A virus (A/equine/Kentucky/9/95 (H3N8))"
/virus
/mol_type="mRNA"
/isolate="A/equine/Kentucky/9/95"
/db_xref="taxon:217810"
/note="H3N8"
1..1061
/gene="HA1"
30..>1061
/gene="HA1"
/codon_start=1
/product="hemagglutinin precursor"
/protein_id="AAF22351.1"
/db_xref="GI:6651515"
/translation="MKTIIILIKLTHWVYSONPTSGNNTATLCLGHAVANGTLVKTI
TDDQIEVNTATLQVSIKIKCNNSRVLDGRNCTLDMLGDPCHCDVFOYENDL
IERSAFNSCTPYDIPYASURSIIVASSGTLEFTAGETFTGVTQNGRSAGCKRSAD
SFFRLNMLTKGNSYPLTNMNNKFDKLYIWIHHPSSNQKOTBELYIOESGRVT
VTRKRSQTIIPNIGSRPWRVGSGRISYIWTIVKPGDILMINSNGNIVAPEGYPLK
TSGSVNRSADIPIDICVSECITPNSIPNDKPFQNVNKTIVKPCPKYIRQNTLKLAT
MRNYPEKQIR"
30..74
/sig_peptide
75..>1061
/mat_peptide
/gene="HA1"
/product="hemagglutinin"
ORIGIN
```

```
Query Match 99.1%; Score 1051.4; DB 14; Length 1061;
Best Local Similarity 99.4%; Pred. No. 1.6e-239;
Matches 1055; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 AGCAAAACAGCGGGATTTCTGTCATCATGACGACCAACCACTATTTTGTACTACTCA 60
Db 1 AGCAAAACAGCGGGATTTCTGTCATCATGACGACCAACCACTATTTTGTACTACTCA 60
QY 61 CCCATTGGGTCTACAGTCAAAACCCCAACCAAGTGGAAACCAACACATTTATGCTGG 120
Db 61 CCCATTGGGTCTACAGTCAAAACCCCAACCAAGTGGAAACCAACACATTTATGCTGG 120
QY 121 GACACCATGAGTAGCAAAATGGACATTTGGTAAACCAATTAATGATGACCAATTTGAGG 180
Db 121 GACACCATGAGTAGCAAAATGGACATTTGGTAAACCAATTAATGATGACCAATTTGAGG 180
QY 181 TGACAAATGCTACTGAAATTTAGTTTACAGACATTTCAATAGGGAATATGCAACACTCAT 240
Db 181 TGACAAATGCTACTGAAATTTAGTTTACAGACATTTCAATAGGGAATATGCAACACTCAT 240
QY 241 ATAAAGTCTTAGATGAAGAAATTTGACATTAATAGATGCAATGCTAGGAGACCCCACT 300
Db 241 ATAGAGTCTTAGATGAAGAAATTTGACATTAATAGATGCAATGCTAGGAGACCCCACT 300
QY 301 GTGATGCTTCCAGTATGAGAAATTTGACATTAATAGATGCAATGCTAGGAGACCCCACT 360
Db 301 GTGATGCTTCCAGTATGAGAAATTTGACATTAATAGATGCAATGCTAGGAGACCCCACT 360
QY 361 ATTGCTACCCCATATGACATCCCTGACTATGATCGCTCGGTCCATTTGAGCATCTCAG 420
Db 361 ATTGCTACCCCATATGACATCCCTGACTATGATCGCTCGGTCCATTTGAGCATCTCAG 420
QY 421 GAACATTAAGAAATTCACAGCAGAGGATTCACATGACAGAGGTCTCACTCAAAACGGAAGA 480
```

QY	61	CCATTGGGCTTACAGTCAAAACCCAACCAAGTGGAAACCAACAGCAGCCACATTATGTCTGG	120
Db	61	CCCATTTGGGCTTACAGTCAAAACCCAACCAAGTGGAAACCAACAGCAGCCACATTATGTCTGG	120
QY	121	GACACCATGAGTAGCAAAATGGGAACATTGGTAAAAACAATACTGATGACCAAAATTTGAGG	180
Db	121	GACACCATGAGTAGCAAAATGGGAACATTGGTAAAAACAATACTGATGACCAAAATTTGAGG	180
QY	181	TGACAAATGCTACTGAATTAGTTAGTCAGAGCAATTTCAATAGGGAATAATATGCAACAACTCAT	240
Db	181	TGACAAATGCTACTGAATTAGTTAGTCAGAGCAATTTCAATAGGGAATAATATGCAACAACTCAT	240
QY	241	ATAAAGTTCTAGATGGGAAGAAATGGCACATTAATAGATGCAATGCTAGGAGACCCCCACT	300
Db	241	ATAAAGTTCTAGATGGGAAGAAATGGCACATTAATAGATGCAATGCTAGGAGACCCCCACT	300
QY	301	GTGATGCTTTCCAGTATGAGAAATGGGACCTCTTCATPAGAAAGAGCAGCGCTTTTCAGCA	360
Db	301	GTGATGCTTTTCAGTATGAGAAATGGGACCTCTTCATPAGAAAGAGCAGCGCTTTTCAGCA	360
QY	361	ATTGCTACCCATATGACATCCCTGACTATGCGATCGCTCCCGTCCATTTGTAGCATCTCAG	420
Db	361	ATTGCTACCCATATGACATCCCTGACTATGCGATCGCTCCCGTCCATTTGTAGCATCTCAG	420
QY	421	GACATTAGAAATTCACAGCAGAGGGATTCACTGGACAGGTGTCTCAAAAACGGGAAGAA	480
Db	421	GACATTAGAAATTCACAGCAGAGGGATTCACTGGACAGGTGTCTCAAAAACGGGAAGAA	480
QY	481	GTGAGAGCTCGAAAAGGGGATCAGCCGATAGTTCTTTTACCGCATGAAATGGCTTAACAA	540
Db	481	GTGAGAGCTCGAAAAGGGGATCAGCCGATAGTTCTTTTACCGCATGAAATGGCTTAACAA	540
QY	541	AATCTGGAAACTCTTACCCACATTGAAATGTGACAAATGCCTTAACAATAAAAAATTCGACA	600
Db	541	AATCTGGAAACTCTTACCCACATTGAAATGTGACAAATGCCTTAACAATAAAAAATTCGACA	600
QY	601	AACATATACATCTGGGGGATTCATCAACCGAGCTCAAAACCAACAGCAGACAGAAATTTGATCA	660
Db	601	AACATATACATCTGGGGGATTCATCAACCGAGCTCAAAACCAACAGCAGACAGAAATTTGATCA	660
QY	661	TCCAAGAAATCAGGACGAGTAAACAGTCTCAACAAAAGAAAGTCAACAAACGATAGTCCCTTA	720
Db	661	TCCAAGAAATCAGGACGAGTAAACAGTCTCAACAAAAGAAAGTCAACAAACGATAGTCCCTTA	720
QY	721	ATATCGGATCTAGACCGTGGGTTAGGGGTCAATCAGCAGGATTAAGCATATACCTGGACCA	780
Db	721	ATATCGGATCTAGACCGTGGGTTAGGGGTCAATCAGCAGGATTAAGCATATACCTGGACCA	780
QY	781	TTGTAAACCTGGAGATATCTTAATGATAAACAGTAAATGGCAACTTAGTTGACCGCGGG	840
Db	781	TTGTAAACCTGGAGATATCTTAATGATAAACAGTAAATGGCAACTTAGTTGACCGCGGG	840
QY	841	GATATTTTAAATTTGAAAACAGGGGAAAAGCTCTGTAATGAGATCAGATGACACCCATAGACA	900
Db	841	GATATTTTAAATTTGAAAACAGGGGAAAAGCTCTGTAATGAGATCAGATGACACCCATAGACA	900
QY	901	TTTGTGCTCTGAATGATTAACCAAAATGGAAGCATCCCCAACGACAAACCATTTCAA	960
Db	901	TTTGTGCTCTGAATGATTAACCAAAATGGAAGCATCCCCAACGACAAACCATTTCAA	960
QY	961	ATGTGAACAAAGTTATCATATGGAATAATGCCCAAGTATATCAGGCAAAAACATTTAAAGC	1020
Db	961	ATGTGAACAAAGTTATCATATGGAATAATGCCCAAGTATATCAGGCAAAAACATTTAAAGC	1020
QY	1021	TGGCCACTGGGATGAGGAATATACCAAGAAAAGCAAAATCAGA	1061
Db	1021	TGGCCACTGGGATGAGGAATATACCAAGAAAAGCAAAATCAGA	1061

RESULT 3  
AF197248  
LOCUS

VRL 08-JAN-2003

1061 bp	mRNA	linear
1061 bp	mRNA	linear

AF197248

AF197248  
LOCUS

/translation="MKTTIILLLTHWVYSONPTSGNNTATLCLGHAVANGTLVTKI  
TDDQIEVNTAYELVQSIGIKCNYSYKVLDRNCTLDMLGDPCHDVOYENWDLF  
IERSAFENYCPYDIPDYASLRSIVASSGTLEPTAEGTWTGVTONGSGACKRSAD  
SFFRLNWLTKSGNSYPTLVNTPNNKPFDKLYIWIHHPSSNOOQTELYIOESGRVT  
VSTRSQOTIIPNIGSRPWRVQSGRISYIWTIVKPGDILMINSNGNLVAPRGYFKLK  
TKGSVMRSADAPIDICVSECITPNSIPNDKPFQNVNVTYKCPKIRQNTLKLATG  
MRNPEKQIR"  
30.74  
sig\_peptide  
75.>1061  
mat\_peptide  
/gene="HA1"  
/product="hemagglutinin"

ORIGIN

Query Match 100.0%; Score 1061; DB 14; Length 1061;  
Best Local Similarity 100.0%; Pred. No. 8,3e-242;  
Matches 1061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCAAAAGCAGGGGATATTCTGTCAATCATGAAGCAACCAATATTTTGTGATCTACTGA 60  
DB 1 AGCAAAAGCAGGGGATATTCTGTCAATCATGAAGCAACCAATATTTTGTGATCTACTGA 60

QY 61 CCCATTGGGTCTACAGTCAAAACCCCAACAGTGGAAACAACACGCCACATTATCTCTGG 120  
DB 61 CCCATTGGGTCTACAGTCAAAACCCCAACAGTGGAAACAACACGCCACATTATCTCTGG 120

QY 121 GACACATGCTAGTCAAAATGAAACATTTGGTAAACCAATATCTGATGACCAAAATTTGAGG 180  
DB 121 GACACATGCTAGTCAAAATGAAACATTTGGTAAACCAATATCTGATGACCAAAATTTGAGG 180

QY 181 TGACAAATGCTACTGAATTTAGTTCAGAGCATTTCAATAGGGAATATGCAACAACTCAT 240  
DB 181 TGACAAATGCTACTGAATTTAGTTCAGAGCATTTCAATAGGGAATATGCAACAACTCAT 240

QY 241 ATAAAGTTCTAGATGGAAGAAATTCGACATTAATAGATCAATGCTAGGAGACCCCACT 300  
DB 241 ATAAAGTTCTAGATGGAAGAAATTCGACATTAATAGATCAATGCTAGGAGACCCCACT 300

QY 301 GTGATGCTCTCCAGTATGAGAAATTTGGACCTCTTCATAGAAAGAGCAGCGCTTTTCAGCA 360  
DB 301 GTGATGCTCTCCAGTATGAGAAATTTGGACCTCTTCATAGAAAGAGCAGCGCTTTTCAGCA 360

QY 361 ATTGCTACCATATGACATCCCTGACTATGATCGCTCCGGTCCATTGTAGCATCTCTCAG 420  
DB 361 ATTGCTACCATATGACATCCCTGACTATGATCGCTCCGGTCCATTGTAGCATCTCTCAG 420

QY 421 GAACATTAGAAATTCACAGCAGAGGGAATTCACATGACAGGTGCTCACTCAAAACGGAAGA 480  
DB 421 GAACATTAGAAATTCACAGCAGAGGGAATTCACATGACAGGTGCTCACTCAAAACGGAAGA 480

QY 481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTCTTTTAGCCGACTGMAATTCGGCTAAACA 540  
DB 481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTCTTTTAGCCGACTGMAATTCGGCTAAACA 540

QY 541 AATCTGGAACCTTTACCCCAATTGAATGTGACAAATGCTTAAACCAATATAAAATTTTCGACA 600  
DB 541 AATCTGGAACCTTTACCCCAATTGAATGTGACAAATGCTTAAACCAATATAAAATTTTCGACA 600

QY 601 AACTATACATCTGGGGATTCATCCCGAGTCAACCAACAGCAGACAGAAATTTGTACA 660  
DB 601 AACTATACATCTGGGGATTCATCCCGAGTCAACCAACAGCAGACAGAAATTTGTACA 660

QY 661 TCCAGAATTCAGGACGAGTAAACAGTCTCAACAAAGAAAGTCAACAAACGATAGTCCCTTA 720  
DB 661 TCCAGAATTCAGGACGAGTAAACAGTCTCAACAAAGAAAGTCAACAAACGATAGTCCCTTA 720

QY 721 ATATCGGATCTAGACCGTGGGTAGGGGTCAATTCAGGCAAGGATAAGCATATATCTGACCA 780  
DB 721 ATATCGGATCTAGACCGTGGGTAGGGGTCAATTCAGGCAAGGATAAGCATATATCTGACCA 780

QY 781 TTGTAAACCTGAGATATCTTAATGATATAACAGTAAATGGCAACTTAGTTGACCGCGGG 840  
DB 781 TTGTAAACCTGAGATATCTTAATGATATAACAGTAAATGGCAACTTAGTTGACCGCGGG 840

QY 841 GATATTTTAAATTTGAAAAACAGGAAAGCTCTGTAATGAGATCAGATGACCCCATAGACA 900  
DB 841 GATATTTTAAATTTGAAAAACAGGAAAGCTCTGTAATGAGATCAGATGACCCCATAGACA 900

QY 901 TTTGTGTCCTGGAATGTATTACCAAAATGGAAGCATCCCCAACGACAAACCATTTTCAA 960  
DB 901 TTTGTGTCCTGGAATGTATTACCAAAATGGAAGCATCCCCAACGACAAACCATTTTCAA 960

QY 961 ATGTGAACAAAGTTTACATATGGAATAATGCCCAAGTATATCAGGCAAAACACATTTTAAAGC 1020  
DB 961 ATGTGAACAAAGTTTACATATGGAATAATGCCCAAGTATATCAGGCAAAACACATTTTAAAGC 1020

QY 1021 TGGCCACTGGGATGAGGAATATACCAAAAAAGCAAAATCAGA 1061  
DB 1021 TGGCCACTGGGATGAGGAATATACCAAAAAAGCAAAATCAGA 1061

RESULT 2  
AY273168  
LOCUS  
DEFINITION  
Influenza A virus (A/equine/Oklahoma/2000 (H3N8)) linear VRL 19-MAR-2004  
precursor (HA1) gene, partial cds.  
ACCESSION  
AY273168  
VERSION  
AY273168.1 GI:33415851  
KEYWORDS  
ORGANISM  
Influenza A virus (A/equine/Oklahoma/2000 (H3N8))  
Influenza A virus (A/equine/Oklahoma/2000 (H3N8))  
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
Influenzavirus A.  
REFERENCE  
1 (bases 1 to 1061)  
AUTHORS  
Lai,A.C.K., Rogers,K.M., Glaser,A., Tudor,L. and Chambers,T.  
TITLE  
Alternate circulation of recent equine-2 influenza viruses (H3N8)  
from two distinct lineages in the United States  
JOURNAL  
Virus Res. 100 (2), 159-164 (2004)  
PUBMED  
15019234  
REFERENCE  
2 (bases 1 to 1061)  
AUTHORS  
Lai,A.C.K.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (10-APR-2003) Microbiology & Molecular Genetics, Oklahoma  
State University, 306 Life Science East, Stillwater, OK 74078, USA  
FEATURES  
source  
1.1061  
/organism="Influenza A virus  
(A/equine/Oklahoma/2000 (H3N8))"  
/virion  
/mol\_type="genomic RNA"  
/isolate="A/Eq/Oklahoma/2000"  
/db\_xref="taxon:241186"  
30..>1061  
/gene="HA1"  
30..>1061  
/gene="HA1"  
/codon\_start=1  
/product="hemagglutinin precursor"  
/protein\_id="AAQ18435.1"  
/db\_xref="GI:33415852"  
/translation="MKTTIILLLTHWVYSONPTSGNNTATLCLGHAVANGTLVTKI  
TDDQIEVNTAYELVQSIGIKCNYSYKVLDRNCTLDMLGDPCHDVOYENWDLF  
IERSAFENYCPYDIPDYASLRSIVASSGTLEPTAEGTWTGVTONGSGACKRSAD  
SFFRLNWLTKSGNSYPTLVNTPNNKPFDKLYIWIHHPSSNOOQTELYIOESGRVT  
VSTRSQOTIIPNIGSRPWRVQSGRISYIWTIVKPGDILMINSNGNLVAPRGYFKLK  
TKGSVMRSADAPIDICVSECITPNSIPNDKPFQNVNVTYKCPKIRQNTLKLATG  
MRNPEKQIR"

ORIGIN

Query Match 99.5%; Score 1056.2; DB 14; Length 1061;  
Best Local Similarity 99.7%; Pred. No. 1.2e-240;  
Matches 1058; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCAAAAGCAGGGGATATTCTGTCAATCATGAAGCAACCAATATTTTGTGATCTACTGA 60  
DB 1 AGCAAAAGCAGGGGATATTCTGTCAATCATGAAGCAACCAATATTTTGTGATCTACTGA 60

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 01:45:21 ; Search time 4887 Seconds  
(without alignments)  
10519.948 Million cell updates/sec

Title: US-10-826-929A-1

Perfect score: 1061

Sequence: 1 agcaaaagcaggggatattt.....taccagaaagcaaatcaga 1061

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

#### Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1061	100.0	1061	14	AF197241 Influenza
2	1056.2	99.5	1061	14	AY273168 Influenza
3	1053	99.2	1061	14	AF197248 Influenza
4	1051.4	99.1	1061	14	AF197247 Influenza
5	1048.2	98.8	1762	14	FLAH33B
6	1043.4	98.3	1060	14	EIVY14059
7	1041.8	98.2	1060	14	EIVY14060
8	1041.8	98.2	1762	14	FLAH33D
9	1039.2	97.9	1100	14	EIVY14058
10	1038.6	97.9	1762	14	FLAH33F
11	1035.4	97.6	1061	14	AF197242
12	1033.8	97.4	1762	6	BD244631
13	1033.8	97.4	1762	6	AR254631
14	1033.8	97.4	1762	6	AR343239
15	1033.8	97.4	1762	6	AR455506
16	1033.8	97.4	1762	14	FLAH33A
17	1032.2	97.3	1762	6	BD244629
18	1032.2	97.3	1762	6	AR254629
19	1032.2	97.3	1762	6	AR343237

20	1032.2	97.3	1762	6	AR455504
21	1030.6	97.1	1061	14	AF197245
22	1030.6	97.1	1762	14	FLAH33E
23	1029	97.0	1061	14	AF197249
24	1027.4	96.8	1762	14	FLAH33C
25	1022.6	96.4	1061	14	AF197243
26	1022.6	96.4	1061	14	AF197244
27	1022.6	96.4	1090	14	EIVY14056
28	1022.6	96.4	1762	14	IYAH691
29	1021.2	96.2	1762	14	IYAH991
30	1019.4	96.1	1061	14	AY273167
31	1019.2	96.1	1032	14	IYAH931
32	1019.2	96.1	1698	6	AR490205
33	1019.2	96.1	1698	6	AX018718
34	1018.4	96.0	1762	6	AR011427
35	1018.4	96.0	1762	6	I18065
36	1016.8	95.8	1762	14	FLAET85HA
37	1016.2	95.8	1762	14	EIVH3A
38	1015.6	95.7	1040	14	FLAH33N8HAD
39	1014.6	95.6	1061	14	AF197246
40	1014.2	95.6	1099	14	FLAH33N8HAJ
41	1011.8	95.4	1093	14	FLAH33N8HAE
42	1010.4	95.2	1762	14	FLAER87HA
43	1008.8	95.1	1762	14	FLAER86HA
44	1007	94.9	1096	14	FLAH33N8HAG
45	1006.6	94.9	1060	14	EIVY14057

#### ALIGNMENTS

RESULT 1	AF197241	AF197241	Influenza A virus (A/equine/Kentucky/1/98 (H3N8))	linear	VRL 08-JAN-2003
LOCUS	AF197241	precursor	(HAI) mRNA, partial cds.		
DEFINITION	AF197241	1061 bp	mRNA		
ACCESSION	AF197241	GI:6651502			
VERSION	AF197241.1				
KEYWORDS					
SOURCE			Influenza A virus (A/equine/Kentucky/1/98 (H3N8))		
ORGANISM			Influenza A virus (A/equine/Kentucky/1/98 (H3N8))		
REFERENCE			Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;		
AUTHORS			1 (bases 1 to 1061)		
TITLE			Lai,A.C.C., Chambers,T.M., Holland,R.E. Jr., Morley,P.S.,		
JOURNAL			Haines,D.M., Townsend,H.G. and Barrandeguy,M.		
MEDLINE			Diverged evolution of recent equine-2 influenza (H3N8) viruses in		
PUBMED			the Western Hemisphere		
REFERENCE			Arch. Virol. 146 (6), 1063-1074 (2001)		
AUTHORS			2 (bases 1 to 1061)		
TITLE			Lai,A.C.K.		
JOURNAL			Submitted (21-OCT-1999) Microbiology & Molecular Genetics, Oklahoma		
MEDLINE			State University, 306 Life Science East, Stillwater, OK 74078, USA		
PUBMED			Location/Qualifiers		
FEATURES			1..1061		
source			/organism="Influenza A virus		
gene			(A/equine/Kentucky/1/98 (H3N8))"		
CDS			/virion		
			/mol_type="mRNA"		
			/isolate="A/equine/Kentucky/1/98"		
			/db_xref="taxon:217817"		
			/note="H3N8"		
			1..>1061		
			/gene="HA1"		
			30..>1061		
			/gene="HA1"		
			/codon_start=1		
			/product="hemagglutinin precursor"		
			/protein_id="AAF22345.1"		
			/db_xref="GI:6651503"		

QY 210 ATTTCAATGGGAAATATGCACAACTCATATAAGTTCTAGATGCAAGAAATTCGACA 269  
Db 61 ILeSerIleGlyLysIleCysAsnAsnProTyrArgValLeuAspGlyArgAsnCysThr 80  
QY 270 TTAATAGATGCAATGCTAGAGACCCCACTGTGATGCTTCCAGTATGAGAAATTCGGAC 329  
Db 81 LeuIleAspAlaMetLeuGlyTyrProHisCysAspValPheGlnTyrGluAsnTrpAsp 100  
QY 330 CTCTTCATGAAGAAGACGCGTTTCAGCAATTCCTACCATATGATCATCCCTGACTAT 389  
Db 101 LeuPheIleGluArgSerThrPheSerAsnCysTyrProTyrAspIleProAspTyr 120  
QY 390 GCATCGCTCCGCTCATTTAGATCTCTCAGAACATTAAGTATCAGAGAGGATTC 449  
Db 121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140  
QY 450 AChTGGACAGTGTCACTCAAAACGGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509  
Db 141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysLysArgGlySerAlaAsp 160  
QY 510 AGTTCTTTTACCGCACTGAATTCGCTAACCAAAATCTGGAACCTTACCCCAATTTGAAT 569  
Db 161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProThrLeuAsn 180  
QY 570 GTGCATATGCTTCACTAAATAAAATTCGACAAATATATCATCTGGGGATTCATCCCG 629  
Db 181 ValThrMetProAsnAsnAsnAsnAspLysLeuTyrIleTrpGlyIleHisPro 200  
QY 630 AGCTCAAAACACAGACAGATTCATCATCAAGAAATTCAGAGAGGATTCAGCTCA 689  
Db 201 SerSerAsnAsnGluGlnThrLysLeuTyrIleGlnLysSerGlyArgValThrValSer 220  
QY 690 ACAAAGAGTCAACAAACGATAGTCCCTTAATTCGGATCTAGACCGTGGTGGGT 749  
Db 221 ThrLysArgSerGlnThrIleIleProAsnIleGlySerArgProGlyIleArgGly 240  
QY 750 CAATCAGCAGGATAGCATATATCTGACCAATTCGAAACCTGGAGATTCCTTAATGATA 809  
Db 241 GlnSerGlyArgIleSerIleTyrTrpIleValLysProGlyAspIleLeuMetVal 260  
QY 810 AACAGTAATGGCACTAGTTCACCGCGGGATATTTAAATTTGAAACAGGGAAGC 869  
Db 261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysMetArgThrGlyLysSer 280  
QY 870 TCTGTATAGATCAGATGACCCATAGACATTTGTGTCTCAATTCGATATTCACCAAT 929  
Db 281 SerValMetArgSerAspAlaProIleAspThrCysValSerGluCysIleThrProAsn 300  
QY 930 GGAAGCATCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTATCATATGGAATGC 989  
Db 301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 320  
QY 990 CCCAAGTATATCAGGCAAAACATTTAAAGTGGCCACTGGGATGAGGATATACAGAA 1049  
Db 321 ProLysTyrIleLysGlnAsnThrLysLeuAlaThrGlyMetArgAsnValProGlu 340  
QY 1050 AAGCAATCAGA 1061  
Db 341 LysGlnIleArg 344

RESULT 6  
HMI7

N:Contains: hemagglutinin HA1; hemagglutinin HA2  
C:Species: influenza A virus  
C>Date: 30-Sep-1990 #sequence\_revision 30-Sep-1990 #text\_change 16-Jul-1999  
R:Kawaoka, Y.; Bean, W.J.; Webster, R.G.  
Virology 169, 283-292, 1989  
A:Title: Evolution of the hemagglutinin of equine H3 influenza viruses.  
A:Reference number: A34064; MUID:89204899; PMID:2705299  
A:Accession: G34064  
A:Molecule type: genomic RNA

A:Residues: 1-565 <KAW>  
A:Cross-references: GB:M24724; GB:J04336; NID:G324014; PIDN:AAA43109.1; PID:G324015  
C:Genetics:

## A:Map position: segment 4

C:Superfamily: influenza virus hemagglutinin  
C:Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:17-344/Product: hemagglutinin HA1 #status predicted <HA1>  
F:345-551/Product: hemagglutinin HA2 #status predicted <HA2>  
F:535-551/Domain: transmembrane #status predicted <TM1>  
F:18,23,37,53,78,180,300,498/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:29-481,67-292,79-91,154-488,296-320/Disulfide bonds: #status predicted  
F:554,561,564/Binding site: palmitate (Cys) (covalent) #status predicted

## Alignment Scores:

Pred. No.:	9,626-140	Length:	565
Score:	1766.00	Matches:	324
Percent Similarity:	97.97%	Conservative:	13
Best Local Similarity:	94.19%	Mismatches:	7
Query Match:	92.36%	Indels:	0
DB:	1	Gaps:	0

US-10-826-929A-1 (1-1061) x HMI7 (1-565)

QY 30 ATGAAGACCAACCATTTTGTACTACTGACCCATGGTCTACAGTCAAAACCCAACC 89  
Db 1 MetLysThrThrIleIleLeuIleLeuLeuThrHisTrpValTyrSerGlnAsnProThr 20  
QY 90 AGTGGAAACACACACCCACATTTGTCTGGGACACCATGCTAGTACAAATGGAACATTG 149  
Db 21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisAlaValAlaAsnGlyThrLeu 40  
QY 150 GTAAAAACAATAACTGATGACCAAAATTTGAGGTGACAAATGCTACTCAATTAGTTTCAGAGC 209  
Db 41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60  
QY 210 ATTTCAATAGGAAATATGCAACATCATATATAAGTTCTAGATGGAAGAAATTCACA 269  
Db 61 ThrSerIleGlyLysIleCysAsnAsnProTyrArgValLeuAspGlyArgAsnCysThr 80  
QY 270 TTAATAGATGCAATGCTAGGACACCCCACTGTGATGCTTCCAGTATGAGAAATTCGGAC 329  
Db 81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyrGluAsnTrpAsp 100  
QY 330 CTCTTCATGAAGAAGACGCGCTTTCAGCAATTCCTACCATATGATCATCCCTGACTAT 389  
Db 101 LeuPheIleGluArgSerSerAlaPheSerAsnCysTyrProTyrAspIleProAspTyr 120  
QY 390 GCATCGCTCCGCTCATTTAGATCTCTCAGAACATTAAGTATTCACAGAGGATTC 449  
Db 121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140  
QY 450 ACATGACAGGTTGTCCTCAAAACGGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509  
Db 141 ThrTrpThrGlyValThrGlnAsnGlyLysSerGlyAlaCysArgArgGlySerAlaAsp 160  
QY 510 AGTTCTTTTACCGCACTGAATTCGCTAACCAAAATCTGGAACCTTACCCCAATTTGAAT 569  
Db 161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProThrLeuAsn 180  
QY 570 GTGCATATGCTTCACTAAATAAAATTCGACAAATATATCATCTGGGGATTCATCCCG 629  
Db 181 ValThrMetProAsnAsnAsnAsnAspLysLeuTyrIleTrpGlyIleHisPro 200  
QY 630 AGCTCAAAACACAGACAGATTCATCATCAAGAAATTCAGAGAGGATTCAGCTCA 689  
Db 201 SerThrAsnAsnGluGlnThrLysLeuTyrValGlnGluLeuGlyArgValThrValSer 220  
QY 690 ACAAAGAGTCAACAAACGATAGTCCCTTAATTCGGATCTAGACCGTGGTGGGT 749  
Db 221 ThrLysArgSerGlnThrIleIleProAsnIleGlySerArgProGlyIleArgGly 240  
QY 750 CAATCAGCAGGATAGCATATATCTGACCAATTCGAAACCTGGAGATTCCTTAATGATA 809

```

Db      241  GlnSerGlyArgIleSerIleTyrTrpThrIleValIysProGlyAspIleLeuMetile 260
QY      810  AACAGTAATGCAACTTAGTTCACCGCGGGGATATTTAAATTCAGAAACAGGAGAAAGC 869
Db      261  AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysMetArgThrGlyLysSer 280
QY      870  TCTGTAAATGAGATCAGATCAGCCCATAGACATTTCTGTGTCCTGGAATGTATTACACCAAT 929
Db      281  SerIleMetArgSerAspAlaProIleAspThrCysValSerGluCysIleThrProAsn 300
QY      930  GGAAGCATCCCAACGACACAAACCAATTTCAAATGTGAACAAAGTTACATATGGAATAATGC 989
Db      301  GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyGluCys 320
QY      990  CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGATGAGGATATACCAAGAA 1049
Db      321  ProLysTyrIleLysGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu 340
QY      1050  AAGCAAAATCAGA 1061
Db      341  LysGlnIleArg 344

```

## RESULT 7

## HMIVE6

hemagglutinin precursor - influenza A virus (strain A/equine/Fontainebleau/76 [H3N8])

N:Contains: hemagglutinin HA1; hemagglutinin HA2

C:Species: Influenza A virus

C>Date: 30-Sep-1990 #sequence\_revision 30-Sep-1990 #text\_change 16-Jul-1999

C:Accession: F34064

R:Kawaoka, Y.; Bean, W.J.; Webster, R.G.

A:Title: Evolution of the hemagglutinin of equine H3 influenza viruses.

A:Reference number: A34064; MUID:89204899; PMID:2705299

A:Accession: F34064

A:Molecule type: genomic RNA

A:Cross-references: GB:M24723; GB:J04336; NID:G323998; PIDN:AAA43101.1; PID:G323999

C:Genetics:

A:Map position: segment 4

C:Superfamily: influenza virus hemagglutinin

C:Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond

F:1-16/Domain: signal sequence #status predicted <SIG>

F:17-344/Product: hemagglutinin HA1 #status predicted <HA1>

F:345-565/Product: hemagglutinin HA2 #status predicted <HA2>

F:535-553/Domain: transmembrane #status predicted <TM1>

F:18,23,37,53,78,180,300,498/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:229,481,67-292,79-91,154-488,296-320/Disulfide bonds: #status predicted

F:554,561,564/Binding site: palmitate (Cys) (covalent) #status predicted

Alignment Scores:

Pred. No.:	1,41e-139	Length:	565
Score:	1764.00	Matches:	325
Percent Similarity:	97.97%	Conservative:	12
Best Local Similarity:	94.48%	Mismatches:	7
Query Match:	92.26%	Indels:	0
DB:	1	Gaps:	0

US-10-826-929a-1 (1-1061) x HMIVE6 (1-565)

```

QY      30  ATGAAGACAAACATTATTTTGATCTACTGACCCATGGGTCTACAGTCAAAACCCAAACC 89
Db      1  MetLysThrThrIleIleLeuLeuLeuThrHisTrpValTyrSerGlnAsnProThr 20
QY      90  AGTGGAAACACACACGCCCATTTATGCTGGGACACCATCGAGTAGCAATGGAACATWG 149
Db      21  SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40
QY      150  GTAATAACAATACTCATGACCAAAATTTAGGTGACAAATGCTACTGAAATTTAGTTCAGAGC 209
Db      41  ValLysThrThrAspAspGlnIleGluValThrAsnAlaThrGlnLeuValGlnSer 60
QY      210  ATTTCATAGGGGAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTCACA 269

```

```

Db      61  ThrSerIleGlyLysIleCysAsnAsnProTyrArgValLeuAspGlyArgAsnCysThr 80
QY      270  TTATAGATCAATGCTAGGAGACCCACCTGTCATGCTCTCCAGTAGTGAATTTGGGAC 329
Db      81  LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyrGluAsnTrpAsp 100
QY      330  CTCTTCATAGAAAGACAGCGCTTTTTCAGCAATTTGCTACCCATATGACATCCCTGACTAT 389
Db      101  LeuPheIleGluArgSerSerAlaPheSerAsnCysTyrProTyrAspIleProAspTyr 120
QY      390  GCATCGCTCCGGTCCATTGTAGCATCTTCAGGAACATTAGAAATTCACAGCAGAGGGATTC 449
Db      121  AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140
QY      450  ACATGGACAGGTGCTCACTCAAAACGGAAGAGTGGAGCTCGCAAAAGGGGATCAGCCGAT 509
Db      141  ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysArgGlySerAlaAsp 160
QY      510  AGTTTCTTTAGCCGACTGAATTTGGCTAACAAAATCTGAAAATCTCTACCCCATATTGAAT 569
Db      161  SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProThrLeuAsn 180
QY      570  GTGACATGCTTAACAATAAATTTTCGACAAACTATACATCTGGGGGATTCATCACCAG 629
Db      181  ValThrMetProAsnAsnAsnAsnPheAspLysLeuTyrIleTrpGlyIleHisPro 200
QY      630  AGCTCAACACCAACAGCAGACAGAAATTTGACATCAAGAAATCAGGACGAGTAACTGCTCA 689
Db      201  SerThrAsnAsnGlnThrLysLeuTyrValGlnLeuGlyArgValThrValSer 220
QY      690  ACAAAAAGAGTCAACAAACCATAGTCTCCTAATATCGGATCTAGACCGTGGGTAGGGGT 749
Db      221  ThrLysArgSerGlnThrIleIleProAsnIleGlySerArgProGlyValArgGly 240
QY      750  CAATCAGCAGGATAAGCATATATCTGGACCATTTGTAACCTTGAGAGATATCTTAATGATA 809
Db      241  GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetile 260
QY      810  AACAGTAATGCAACTTAGTTCACCGCGGGGATATTTAAATTCAGAAACAGGAGAAAGC 869
Db      261  AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysMetArgThrGlyLysSer 280
QY      870  TCTGTAAATGAGATCAGATGACCCATGACATTTTGTGTCTGATGATTTATACACCAAT 929
Db      281  SerIleMetArgSerAspAlaProIleAspThrCysValSerGluCysIleThrProAsn 300
QY      930  GGAAGCATCCCAACGACACAAACCAATTTCAAATGTGAACAAATGACAAATGGAATGCA 989
Db      301  GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 320
QY      990  CCCAAGTATATCAGGCAAAACCACTTTAAAGCTGGCCACTGGATGAGGATATACCAAGAA 1049
Db      321  ProLysTyrIleLysGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu 340
QY      1050  AAGCAAAATCAGA 1061
Db      341  LysGlnIleArg 344

```

## RESULT 8

## HMIVE6

hemagglutinin precursor - influenza A virus (strain A/equine/New Market/76 [H3N8])

N:Contains: hemagglutinin HA1; hemagglutinin HA2

C:Species: Influenza A virus

C>Date: 30-Sep-1990 #sequence\_revision 30-Sep-1990 #text\_change 16-Jul-1999

C:Accession: E34064

R:Kawaoka, Y.; Bean, W.J.; Webster, R.G.

A:Title: Evolution of the hemagglutinin of equine H3 influenza viruses.

A:Reference number: A34064; MUID:89204899; PMID:2705299

A:Accession: E34064

A:Molecule type: genomic RNA

A:Residues: 1-565 <KAW>



```
Db      61 ThrSerThrGlyLysIleCysAsnAsnProTyrArgValLeuAspGlyArgAsnCysThr 80
QY      270 TTAATAGATGCAATGCTAGGAGACCCCACTGCTGATGCTTCCAGTATCAGAAATGGGAC 329
Db      81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyrGlyAsnTrpAsp 100
QY      330 CTCTTCATAGAAGAAGCAGCGCTTACCAATTCCTACCCATATGACATCCCTCAGCAT 389
Db      101 LeuPheIleGluArgSerAlaPheSerAsnCysTyrProTyrAspIleProAspTyr 120
QY      390 GCATCGCTCCGCTCATTGTAGCATCTCAGGAACATTAGAAATTCACAGCAGAGGATTC 449
Db      121 AlaSerLeuArgSerLeuValAlaSerSerGlyThrLeuGluPheMetAlaGluGlyPhe 140
QY      450 ACATGACAGGTGTCTACTCAAAACGGAAGAAGTGGAGCTGCAAAAGGGGATCAGCCGAT 509
Db      141 ThrTrpThrGlyValThrGlnAsnGlyArgSerSerAlaCysArgGlySerAlaAsp 160
QY      510 AGTTTCTTTAGCGGACTGAATTTGGCTTAACAAATCTGGAACCTCTTACCCACATTTGAAT 569
Db      161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProThrLeuAsn 180
QY      570 GTGCAATCCCTAAACAATAAATTTTCGACAACTATATCATCTGGGGGATTCATCACCGG 629
Db      181 ValThrMetProAsnAsnAspAsnPheAspLysLeuTyrIleTrpGlyIleHisPro 200
QY      630 AGCTCAACCAACAGCAGACAGAAATGTATCATCCAAAGATCAGGACGAGTAAACAGTCTCA 689
Db      201 SerThrAsnAsnGluGlnThrLysLeuTyrValGlnAlaSerGlyArgValThrValSer 220
QY      690 ACAAAGAAGTCAACAAACGATAGTCCCTTAATATCGGATCTAGACCGTGGGTAGGGGT 749
Db      221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProTrpValArgGly 240
QY      750 CAATCAGCAGGATAGCATATATCTGACCAATTTGTAACACCTGGAGATATCTTAATGATA 809
Db      241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspValLeuMetIle 260
QY      810 AACAGTAATGGCACTTACTGACCGCGGGATATTTTAAATTTAAACAGGGAAGAC 869
Db      261 AsnSerAsnGlyAsnLeuIleAlaProArgGlyTyrPheLysMetArgThrGlyLysSer 280
QY      870 TCTGTAATCAGATCAGATCCACCATAGACATTTGCTGCTCGAATGTAATACCAAT 929
Db      281 SerIleMetArgSerAspAlaProIleAspThrCysValSerGluCysIleThrProAsn 300
QY      930 GGAAGCATCCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACATATGGAATGC 989
Db      301 GlySerIleProAsnAsnLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 320
QY      990 CCCAGTATATCAGGCAAAACACTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1049
Db      321 ProLysTyrValLysGlnSerThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu 340
QY      1050 AAGCAATCAGA 1061
Db      341 ArgGlnIleArg 344
```

## RESULT 10

```
HMIVE2
hemagglutinin precursor - influenza A virus (strain A/equine/Miami/1/63 [H3N8])
N:Contains: hemagglutinin HA1; hemagglutinin HA2
C:Species: influenza A virus
C:Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
C:Accession: B34064
R:Kawakita, Y.; Bean, W.J.; Webster, R.G.
Virology 169, 283-292, 1989
A:Title: Evolution of the hemagglutinin of equine H3 influenza viruses.
A:Reference number: A34064; PMID:89204899; PMID:2705299
A:Accession: B34064
A:Molecule type: genomic RNA
A:Residues: 1-565 <RAW>
A:Cross-references: GB:M24719; GB:J04336; NID:g324006; PIDN:AAA43105.1; PID:g324007
```

```
C:Genetics:
A:Map position: segment 4
C:Superfamily: influenza virus hemagglutinin
C:Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-344/Product: hemagglutinin HA1 #status predicted <HA1>
F:345-565/Product: hemagglutinin HA2 #status predicted <HA2>
F:535-551/Domain: transmembrane #status predicted <TM1>
F:18,23,37,53,78,180,300,496/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:29-481,67-292,154-488,296-320/Disulfide bonds: #status predicted
F:554,561,564/Binding site: palmitate (Cys) (covalent) #status predicted

Alignment Scores:
Pred. No.: 3 86e-134 Length: 565
Score: 1699.00 Matches: 309
Percent Similarity: 95.93% Conservative: 21
Best Local Similarity: 89.83% Mismatches: 14
Query Match: 88.86% Indels: 0
DB: 1 Gaps: 0
```

US-10-826-929A-1 (1-1061) x HMIVE2 (1-565)

```
QY      30 ATGAAGACAACCACTATTATTTGATACTACTGACCCATGGGTCTACAGTCACAAACCCAAACC 89
Db      1 MetLysThrThrThrIleLeuIleLeuLeuThrHisTrpValHisSerGlnAsnProThr 20
QY      90 AGTGAACAACAACAGCAGCCACATTTATCTGGGACACCATGACGACGAAATGGACATTG 149
Db      21 GlyGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40
QY      150 GTAAAAACAATACTGATGACCAATTCAGGTGACAAATGCTACTGAAATTAAGTTTCAGAGC 209
Db      41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60
QY      210 ATTTCAATAGGAAAAATATGCAACATCATATAAAGTTCTAGATGGAAGAAATTCACA 269
Db      61 ThrSerThrGlyLysIleCysAsnAsnProTyrArgValLeuAspGlyArgAsnCysThr 80
QY      270 TTAATAGATGCAATGCTAGGAGACCCCACTGCTGATGCTTCCAGTATGAGAAATGGGAC 329
Db      81 LeuIleAspAlaMetLeuGlyAspProHisTyrAspValPheGlnTyrGluAsnTrpAsp 100
QY      330 CTCTTCATAGAAGAAGCAGCGCTTACCAATTCCTACCCATATGACATCCCTCAGCAT 389
Db      101 LeuPheIleGluArgSerSerAlaPheSerAsnCysTyrProTyrAspValProAspTyr 120
QY      390 GCATCGCTCCGCTCATTGTAGCATCTCAGGAACATTAGAAATTCACAGCAGAGGATTC 449
Db      121 AlaSerLeuArgSerLeuValAlaSerSerGlyThrLeuGluPheMetAlaGluGlyPhe 140
QY      450 ACATGACAGGTGTCTACTCAAAACGGAAGAAGTGGAGCTGCAAAAGGGGATCAGCCGAT 509
Db      141 ThrTrpThrGlyValThrGlnAsnGlyGlySerSerAlaCysArgGlySerAlaAsp 160
QY      510 AGTTTCTTTAGCGGACTGAATTTGGCTTAACAAATCTGGAACCTCTTACCCACATTTGAAT 569
Db      161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProThrLeuAsn 180
QY      570 GTGCAATCCCTAAACAATAAATTTTCGACAACTATATCATCTGGGGGATTCATCACCGG 629
Db      181 ValThrMetProAsnAsnAspAsnPheAspLysLeuTyrIleTrpGlyIleHisPro 200
QY      630 AGCTCAACCAACAGCAGACAGAAATGTATCATCCAAAGATCAGGACGAGTAAACAGTCTCA 689
Db      201 SerThrAsnAsnGluGlnThrLysLeuTyrValGlnAlaSerGlyArgValThrValSer 220
QY      690 ACAAAGAAGTCAACAAACGATAGTCCCTTAATATCGGATCTAGACCGTGGGTAGGGGT 749
Db      221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProTrpValArgGly 240
QY      750 CAATCAGCAGGATAGCATATATCTGACCAATTTGTAACACCTGGAGATATCTTAATGATA 809
Db      241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspValLeuMetIle 260
```

[illegible]

QY	270	TTAATAGATGCAATGCTAGGAGACCCCACTGTGATGCTTCCAGTATGAGAAATGGGAC	320
Db	81	LeuileAepAlaMetLeuGlyAAspProHisCysAAspValPheGlnTyrgluAenTrpAep	100
QY	330	CTCTTCATAGAAAGNAGCAGCGCTTTCAGCAATTGCTACCCATATGACATCCCTGACATAT	389
Db	101	LeuPheValGluArgSerSerAlaPheSerAAsnCysTyPrProTyzAspValProAspTy	120
QY	390	GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAAATTCACAGCAGAGGGAATTC	449
Db	121	AlaserLeuArgSerIleValAlaserSerGlyThrLeuGluPheMetAlaGluGlyPhe	140
QY	450	ACATGACAGGTGTCATCTCAAAAAGGAAAGTGGAGCGCTCGAAAAGGGGATTCAGCCGAT	509
Db	141	ThrTrpThrGlyValThrGlnAsnGlyArgSerSerCysArgGlySerAlaAAsp	160
QY	510	AGTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGAAACTCTTACCCACACATTGAAT	569
Db	161	SerPhePheSerArgLeuAenTrpLeuThrLysSerGluSerSerTySerThrLeuAAsn	180
QY	570	GTGCAATTCGCTTAACAATAAAATTTTCGACAAACTATACATCTCGGGGATTCATCACCCG	629
Db	181	ValThrMetProAAsnAAspAAsnPheAAspLysLeuTyrlleTrpGlylleHisHsPro	200
QY	630	AGCTCAAAACCAACAGCAGACAGAAATTGTATCCAAAGAAATCAGACGAGTAACTGCTCA	689
Db	201	SerThrAAsnAAsnGluGlnThrLysLeuTyValGlnAlaserGlyArgValThrValSer	220
QY	690	ACAAAAGAAGTCAACAAACATAGTCCTTAATATCGGATCTAGACCGTGGTTAGGGGT	749
Db	221	ThrLysArgSerGlnGlnThrIleLeuProAAsnIleGlySerArgProTrpValArgGly	240
QY	750	CAATCAGCAGGATAAGCATATATCTGGACCACTTGTAACACCTGGAGATATCTCAATGATA	809
Db	241	GlnSerGlyArgIleSerIleTyTrpThrIleValLysProGlyAspValLeuValIle	260
QY	810	AACAGTAATGCAACTAGTTGTCACCGCGGGGATTTTAAATTCGAAAACAGGGNAAGC	869
Db	261	AAsnSerAAsnGlyAAsnLeuIleAlaProArgGlyTyPrPheLysMetArgAlaGlyLysSer	280
QY	870	TCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTCTGTAATGTATTACACCAAT	929
Db	281	SerIleMetArgSerAspAlaProIleAspThrCysValPheGluCysIleThrProAAsn	300
QY	930	GGAAAGCATCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACATATGGAATAATGC	989
Db	301	GlySerIleProAAsnAspLysProPheGlnAAsnValAAsnLysIleThrTyrglyLysCys	320
QY	990	CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGATGAGGAATAATACCAGAA	1049
Db	321	ProLysTyValLysGlnSerThrLeuLysLeuAlaThrGlyMetArgAAsnValProGlu	340
QY	1050	AAGCAAAATCAGA	1061
Db	341	LysArgLeuArg	344
RESULT 12			
HMIVE3			
hemagglutinin precursor - influenza A virus (strain A/equine/Tokyo/71 [H3N8])			
N:Contains: hemagglutinin HA1; hemagglutinin HA2			
C:Species: influenza A virus			
C:Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999			
C:Accession: C34064			
F:Kawaoka, Y.; Bean, W.J.; Webster, R.G.			
Virology 169, 283-292, 1989			
A:Title: Evolution of the hemagglutinin of equine H3 influenza viruses.			
A:Reference number: A34064; MUID:89204899; PMID:2705299			
A:Accession: C34064			
A:Molecule type: genomic RNA			
A:Residues: 1-565 <KAW>			
A:Cross-references: GB:M24720; GB:J04336; NID:g324018; PIDN:AAA43111.1; PID:g33			
G:Genetics:			

A: Map position: segment 4  
C: Superfamily: influenza virus hemagglutinin  
C: Keywords: glycoprotein; hemagglutinin; lipoprotein; thiolester bond  
F: 1-16/Domain: signal sequence #status predicted <SIG>  
F: 17-344/Product: hemagglutinin HA1 #status predicted <HA1>  
F: 345-565/Product: hemagglutinin HA2 #status predicted <HA2>  
F: 535-551/Domain: transmembrane #status predicted <TM1>  
F: 23, 37, 53, 68, 78, 180, 300, 498/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F: 23, 481, 67-232, 79-91, 154-488, 296-320/Disulfide bonds: #status predicted  
F: 554, 561, 564/Binding site: palmitate (Cys) (covalent) #status predicted

Alignment Scores:	
Pred. No.:	3.28e-130
Score:	1652.00
Percent Similarity:	94.77%
Best Local Similarity:	86.34%
Query Match:	86.40%
DB:	1
	Gaps: 0
	Indels: 0
	Mismatches: 18
	Conservative: 29
	Matches: 297
	Length: 565



Db 284 ProAsnGlySerIleProAsnAspLysProPheGlnAsnValAsnLysIleThrTyrgly 303  
QY 984 AAATGCCCAAGTATATACAGGCAAAACACATTTAAAGCTGGCCACCTGGGATGAGGAATATA 1043  
Db 304 AlaCysProLysTyrrValLysGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnVal 323  
QY 1044 CCAGAAAAGCAAAATCAGA 1061  
Db 324 ProGluLysGlnThrArg 329

RESULT 15  
HMIV15  
hemagglutinin precursor - influenza A virus (strain A/duck/Hokkaido/10/85) (fragment)  
N:Contains: hemagglutinin HA1; hemagglutinin HA2  
C:Species: Influenza A virus  
C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 16-Jul-1999  
C:Accession: G27813  
R:Kida, H.; Kawabata, Y.; Naeve, C.W.; Webster, R.G.  
Virology 159, 109-119, 1987  
A:Title: Antigenic and genetic conservation of H3 influenza virus in wild ducks.  
A:Reference number: A94363; MUID:87265458; PMID:2440178  
A:Accession: G27813  
A:Molecule type: Genomic RNA  
A:Residues: 1-550 <KID>  
A:Cross-references: GB:M16743; NID:G324093; PIDN:AAA43149.1; PID:G324094  
C:Genetics:  
A:Map position: segment 4  
C:Superfamily: influenza virus hemagglutinin  
C:Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond  
F:1-328/Product: hemagglutinin HA1 #status predicted <HA1>  
F:320-536/Product: hemagglutinin HA2 #status predicted <HA2>  
F:520-536/Domains: transmembrane #status predicted <TM1>  
F:8,22,38,165,285,483/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:14-466,52-277,64-76,139-473,281-305/Disulfide bonds: #status predicted  
F:539,546,549/Binding site: palmitate (Cys) (covalent) #status predicted

Alignment Scores:  
Pred. No.: 1-36e-120 Length: 550  
Score: 1537.00 Matches: 272  
Percent Similarity: 92.94% Conservative: 31  
Best Local Similarity: 83.44% Mismatches: 23  
Query Match: 80.39% Indels: 0  
DB: 1 Gaps: 0

US-10-826-929A-1 (1-1061) x HMIV15 (1-550)

QY 84 CCAACAGCTGGAAACACACAGCCACATTTGCTGGGACACATGCTAGTACCAATGGA 143  
Db 4 ProGlyAsnAspAsnSerThrAlaThrLeuCysLeuGlyHisHisAlaValProAsnGly 23  
QY 144 ACATTTGTTAAACATTAATGATGACCAAAATTTGAGGTGACAAATCCTACTGTAATGTT 203  
Db 24 ThrLeuValIleThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuVal 43  
QY 204 CAGAGCATTTCAATAGGGAATAATATGCAACAACTCATATATAAGTTCTAGATGAAAGAAAT 263  
Db 44 GlnSerSerSerThrGlyLysIleCysAsnAsnProHisArgIleLeuAspGlyArgAsp 63  
QY 264 TGACATTAATAGATGCAATGCTAGGAGACCCCACTGATGATGCTCTTCAGTATGAGAAAT 323  
Db 64 CysThrLeuIleAspAlaLeuLeuGlyAspProHisCysAspValPheGlnAspGluThr 83  
QY 324 TGGGACCTCTTCATAGAAAGAGACGCGCTTTTCAGCAATTTGCTACCATATGACATCCCT 383  
Db 84 TrpAspLeuPheValGluArgSerAsnAlaPheSerAsnCysTyrrProTyrrAspValPro 103  
QY 384 GACTATGCTATCGCTCCGGTCCATTTAGCATCTCTCAGGAACATTTAGAAATTCAGCAGAG 443  
Db 104 AspTyrrAlaSerLeuArgSerLeuValAlaSerSerGlyThrLeuGluPheIleThrGlu 123  
QY 444 GGATTCACATGGACGCTGCTACTCAAAACGGAGAAAGTGGAGCGCTGCAAAAGGGGATCA 503  
Db 124 GlyPheThrTrpThrGlyValThrGlnAsnGlyGlySerAsnAlaCysLysArgGlyPro 143

QY 504 GCCGATAGTTCTTTAGCCGACTGAATTTGGCTTAACAAAATCTGGAACACTCTTACCCACA 563  
Db 144 AsnSerGlyPhePheSerArgLeuAsnTrpLeuThrLysSerGlySerThrTyrrProVal 163  
QY 564 TTGAATGTGACAAATGCCCTTAACAATAAAATTTCCGACAAACTATACATCTGGGGGATTCAT 623  
Db 164 LeuAsnValThrMetProAsnAsnAspAsnPheAspLysLeuTyrrIleTrpGlyValHis 183  
QY 624 CACCGAGCTCAAACCAACAGACAGACAAATTTGATCATCCAAAGATCAGGACGAGTAACA 683  
Db 184 HisProSerThrAsnGlnGluThrAsnLeuTyrrValGlnAlaSerGlyArgValThr 203  
QY 684 GTCTCAACAAAAGAAAGTCAACAAACGATAGTCCCTAATATATCGGATCTAGACCGTGGTT 743  
Db 204 ValSerThrArgArgSerGlnGlnThrIleIleProAsnIleGlySerArgProTrpVal 223  
QY 744 AGGGTCAATCAGCGCAGGATAAGCATATATCTGGACCATTTGTAAACCTGGAGATATCTTA 803  
Db 224 ArgGlyGlnSerGlyArgIleSerIleTyrrTrpThrValValLysProGlyAspValLeu 243  
QY 804 ATGATAACAGTAATGGCAACTTAGTTCACCGCGGGGATATTTTAAATTTGAAACACAGG 863  
Db 244 VallileAsnSerAsnGlyAsnLeuIleAlaProArgGlyTyrrPheLysMetArgThrGly 263  
QY 864 AAAAGCTCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTCTCTGAATGTATTACA 923  
Db 264 LysSerSerIleMetArgSerAspAlaProIleAspThrCysIleSerGluCysIleThr 283  
QY 924 CCAATGGAAGCATCCCCCAACGACAAACCATTTTCAAAATGTGAAACAAAGTTACATATGA 983  
Db 284 ProAsnGlySerIleProAsnAspLysProPheGlnAsnValAsnLysIleThrTyrgly 303  
QY 984 AAATCCCCCAAGTATATCAGCAGAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATA 1043  
Db 304 AlaCysProLysTyrrValLysGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnVal 323

1044 CCAGAAAAGCAAAATCAGA 1061  
324 ProGluLysGlnThrArg 329

Search completed: February 27, 2005, 18:33:50  
Job time : 59 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: February 27, 2005, 18:07:19 ; Search time 217 Seconds  
(without alignments)  
5007.521 Million cell updates/sec

Title: US-10-826-929A-1  
Perfect score: 1912  
Sequence: 1 agcaaaagcagggatattt.....taccagaaagcaaatcaga 1061

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DSV=xlp  
-O=/cpn2.1/USPTO.spool\_p/US10826929/runat 27022005 095242 27584/app query.fasta\_1.1223  
-DB=UniProt\_03 -GFMT=fasta -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10826929 @CGN 1.1 244 @runat 27022005 095242 27584 -ICPU=3  
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPEXT=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1836	96.0	344	2 Q906P2	Q906P2 influenza a
2	1832	95.8	344	2 Q6WRT8	Q6WRT8 influenza a
3	1831	95.8	344	2 Q82846	Q82846 influenza a
4	1831	95.8	565	2 Q67103	Q67103 influenza a
5	1827	95.6	344	2 Q906N5	Q906N5 influenza a
6	1827	95.6	344	2 Q906N6	Q906N6 influenza a
7	1822	95.3	346	2 Q56857	Q56857 influenza a
8	1822	95.3	346	2 Q56858	Q56858 influenza a
9	1816	95.0	565	2 Q67105	Q67105 influenza a
10	1813	94.8	362	2 Q9YJV1	Q9YJV1 influenza a
11	1813	94.8	565	2 Q67102	Q67102 influenza a
12	1813	94.8	565	2 Q67107	Q67107 influenza a
13	1812	94.8	344	2 Q906P1	Q906P1 influenza a
14	1810	94.7	565	2 Q67106	Q67106 influenza a
15	1808	94.6	344	2 Q906N8	Q906N8 influenza a
16	1808	94.6	565	2 Q82793	Q82793 influenza a

17	1806	94.5	344	2 Q82843	Q82843 influenza a
18	1806	94.5	344	2 Q906N7	Q906N7 influenza a
19	1806	94.5	565	1 HEMA_IHAK7	P17001 influenza a
20	1805	94.4	565	1 HEMA_IHAK7	P16996 influenza a
21	1804	94.4	565	2 Q67104	Q67104 influenza a
22	1803	94.3	343	2 Q9YJV7	Q9YJV7 influenza a
23	1803	94.3	344	2 Q906P0	Q906P0 influenza a
24	1803	94.3	362	2 Q9YJV6	Q9YJV6 influenza a
25	1803	94.3	363	2 Q9YJV4	Q9YJV4 influenza a
26	1799	94.1	357	2 Q56856	Q56856 influenza a
27	1798	94.0	344	2 Q6WRT9	Q6WRT9 influenza a
28	1798	94.0	354	2 Q12292	Q12292 influenza a
29	1797	94.0	344	2 Q906N4	Q906N4 influenza a
30	1797	94.0	344	2 Q906N9	Q906N9 influenza a
31	1795	93.9	353	2 Q12294	Q12294 influenza a
32	1795	93.9	362	2 Q9YJV9	Q9YJV9 influenza a
33	1795	93.9	565	1 HEMA_IHAK7	Q08011 influenza a
34	1794	93.8	565	1 HEMA_IHAK6	P19699 influenza a
35	1794	93.8	565	2 Q82792	Q82792 influenza a
36	1786	93.4	344	2 Q82844	Q82844 influenza a
37	1786	93.4	565	2 Q6TXB8	Q6TXB8 influenza a
38	1785	93.4	346	2 Q56855	Q56855 influenza a
39	1784	93.3	344	2 Q82848	Q82848 influenza a
40	1784	93.3	360	2 Q9YJV8	Q9YJV8 influenza a
41	1781	93.1	359	2 Q9YJV5	Q9YJV5 influenza a
42	1779	93.0	565	2 Q66752	Q66752 influenza a
43	1778	93.0	565	2 Q82559	Q82559 influenza a
44	1776	92.9	344	2 Q82847	Q82847 influenza a
45	1775	92.8	344	2 Q82845	Q82845 influenza a

## ALIGNMENTS

RESULT 1

Q906P2 PRELIMINARY; PRT; 344 AA.  
ID Q906P2  
AC Q906P2  
DT 01-MAY-2000 (TREMREL. 13, Created)  
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)  
DT 01-MAR-2004 (TREMREL. 26, Last annotation update)  
DE Hemagglutinin precursor (Fragment).  
GN Name:HA1;  
OS Influenza A virus (A/equine/Kentucky/1/98 (H3N8)).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenzavirus A; H3N8 subtype.  
OX NCBI\_TaxID=217817;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21395169; PubMed=11504416;  
RA Lai A.C., Chambers T.M., Holland R.E. Jr., Morley P.S., Haines D.M.,  
RA Townsend H.G., Barrandeguy M.;  
RT "Diverged evolution of recent equine-2 influenza (H3N8) viruses in the  
RT Western Hemisphere";  
RL Arch. Virol. 146:1063-1074(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Lai A.C.K.;  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Hemagglutinin is responsible for attaching the virus to  
CC cell receptors and for initiating infection (By similarity).  
CC -!- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains  
CC (HA1 and HA2) linked by a disulfide bond (By similarity).  
CC -!- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.  
DR EMBL; AF197241; AAF22345.1; -;  
DR HSSP; P03437; 2VIU.  
DR GO; GO:0019031; C:Viral envelope; IEA.  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR008980; Capsid hemag.  
DR InterPro; IPR001364; Hemagglutn.  
DR InterPro; IPR000149; Hemagglutn.  
DR Fram; PF00509; Hemagglutinin; 1.  
DR PRINTS; PR00330; HEMAGGLUTN1.  
DR PRINTS; PR00329; HEMAGGLUTN12.

DR ProDom; PD000225; Hemagglutn; 1.  
 KW Envelope protein; Glycoprotein; Hemagglutinin; Signal.  
 FT SIGNAL 1 15 Potential  
 FT CHAIN 16 >344 hemagglutinin.  
 FT NON\_TER 344 344  
 SQ SEQUENCE 344 AA; 38280 MW; D5A49D574FB785ED CRC64;

## Alignment Scores:

Pred. No.: 1,51e-148 Length: 344  
 Score: 1836.00 Matches: 344  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 96.03% Indels: 0  
 DB: 2 Gaps: 0

US-10-826-929A-1 (1-1061) x 09Q6P2 (1-344)

QY 30 ATGAGAACACCACTATTATTGATACCTACTAGCCCTGGTCTACAGTCAAAACCAACC 89  
 Db |||||  
 1 MetLysThrThrIleIleLeuLeuLeuThrHisTprValTy-SerGlnAsnProThr 20  
 QY 90 AGTGGAACAACACAGCCACATTATGCTGGGACACCATGCGAGTACGAAATGGAACATG 149  
 Db |||||  
 21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40  
 QY 150 GTAAAAACAATAACTGATGACCAATTTGAGGTGACAAATGCTACTCAATTACTCAGGC 209  
 Db |||||  
 41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60  
 QY 210 ATTTCATAGGGAATAATGCAACACTCATATATAAGTTCTAGATGGAGAAATGCACA 269  
 Db |||||  
 61 IleSerIleGlyIleCysAsnAsnSerTyrLysValLeuAspGlyArgAsnCysThr 80  
 QY 270 TTAATAGATGCAATGCTAGAGACCCCACTGTGATGCTTCCAGTATGAGAAATGGGAC 329  
 Db |||||  
 81 LeuIleAspAlaMetLeuGlyAspP-ohisCysAspValPheGlnTyrGluAsnTrpAsp 100  
 QY 330 CTCTTCATAGAAGACAGCGCTTTCAGCAATGCTACCCATATGACATCCCTCAGCAT 389  
 Db |||||  
 101 LeuPheIleGluArgSerSerAlaPheSerAsnCysTyrProTyrAspIleProAspTyr 120  
 QY 390 GCATCGCTCCGGTCACTTGTAGCATCTCTCAGGAACATTAGAATTCACAGCAGAGGATTC 449  
 Db |||||  
 121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140  
 QY 450 ACATGACAGGTGTCTACTCAAAACGGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509  
 Db |||||  
 141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysLysArgGlySerAlaAsp 160  
 QY 510 AGTTTCTTTAGCGGACTGATGGCTAACAAATCTGGAACCTTACCCCACTTGAT 569  
 Db |||||  
 161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerSerGlyAsnSerTyrProThrLeuAsn 180  
 QY 570 GTGCAATCCCTAACAAATAAATTCGACAAACTATACATCTGGGGGATTCATCACCOC 629  
 Db |||||  
 181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleTrpGlyIleHisPro 200  
 QY 630 AGCTCAAAACAACAGCAGACAGATTGTCATCCAAAGATCAGGACGAGTAAACAGTCTCA 689  
 Db |||||  
 201 SerSerAsnGlnGlnThrGluLeuTyrIleGlnGluSerGlyArgValThrValSer 220  
 QY 690 ACAAAAGAGTCAACAAACGATGCTCCCTAATATCGGATCTAGACCGGGGTAGGGGT 749  
 Db |||||  
 221 ThrLysArgSerGlnThrIleValProAsnIleGlySerArgProTrpValArgGly 240  
 QY 750 CAATCAGGAGGATAGCATATCTAGCACTTGTAAACACCTGGAGATATCTTAATGATA 809  
 Db |||||  
 241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle 260  
 QY 810 AACAGTAATGGCACTTAGTTCACCGCGGGGATATTTAAATTTGAAAACAGGGAAGC 869  
 Db |||||  
 261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuLysThrGlyLysSer 280

QY 870 TCTGTAATGAGATCAGATGACCCCATAGACATTTGTGTCTGAATGATTACACCAAT 929  
 Db |||||  
 281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn 300  
 QY 930 GGAAGCATCCCAACGACAAACCATTTCAAATGTGAACAAAGTTACATATGGAATAATGC 989  
 Db |||||  
 301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 320  
 QY 990 CCCAGTATATCAGCCAAACACATTTAAAGCTGGCCACTGGGATGAGCAATATACAGAA 1049  
 Db |||||  
 321 ProLysTyrIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnIleProGlu 340  
 QY 1050 AAGCAAAATCAGA 1061  
 Db |||||  
 341 LysGlnIleArg 344

## RESULT 2

Q6WRT8 PRELIMINARY; PRT; 344 AA.  
 AC Q6WRT8;  
 DT 05-JUL-2004 (TREMREL. 27, Created)  
 DT 05-JUL-2004 (TREMREL. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMREL. 27, Last annotation update)  
 DE Hemagglutinin (Fragment).  
 GN Name=HA1;  
 OS Influenza A virus (A/equine/Oklahoma/2000 (H3N8)).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenzavirus A; H3N8 subtype.  
 OX NCBI\_TaxID=241186;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15019234; DOI=10.1016/j.virusres.2003.11.019;  
 RA Lai A.C.K., Rogers K.M., Glaser A., Tudor L., Chambers T.;  
 RT "Alternate circulation of recent equine-2 influenza viruses (H3N8)  
 from two distinct lineages in the United States.";  
 RL Virus Res. 100:159-164(2004).  
 CC -|- FUNCTION: Hemagglutinin is responsible for attaching the virus to  
 cell receptors and for initiating infection (By similarity).  
 CC -|- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains  
 (HA1 and HA2) linked by a disulfide bond (By similarity).  
 CC -|- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.  
 DR EMBL; AY273168; AAQ18435.1; -.  
 DR GO; GO:0019031; C:Viral envelope; IEA.  
 DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
 DR InterPro; IPR008980; Capsid hemag.  
 DR InterPro; IPR001364; Hemagglutn.  
 DR InterPro; IPR000149; Hemagglutn.1.  
 DR Pfam; PF00509; Hemagglutinin; 1.  
 DR PRINTS; PR00330; HEMAGGLUTN1.  
 DR PRINTS; PR00329; HEMAGGLUTN12.  
 DR ProDom; PD000225; Hemagglutn; 1.  
 KW Envelope protein; Glycoprotein; Hemagglutinin.  
 FT NON\_TER 344 344  
 SQ SEQUENCE 344 AA; 38281 MW; DSACB577479FA5ED CRC64;

Alignment Scores:  
 Pred. No.: 3,33e-148 Length: 344  
 Score: 1832.00 Matches: 343  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.71% Mismatches: 0  
 Query Match: 95.82% Indels: 0  
 DB: 2 Gaps: 0

US-10-826-929A-1 (1-1061) x Q6WRT8 (1-344)

QY 30 ATGAGAACACCACTATTATTGATACCTACTAGCCCTGGTCTACAGTCAAAACCAACC 89  
 Db |||||  
 1 MetLysThrThrIleIleLeuLeuLeuThrHisTprValTy-SerGlnAsnProThr 20  
 QY 90 AGTGGAACAACACAGCCACATTATGCTGGGACACCATGCGAGTACGAAATGGAACATG 149  
 Db |||||  
 21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40





```

QY 750 CAATCAGGCGAGGATAAGCATATATCTGACCAATTTGTAACCTGGAGATATCCTAATGATA 809
Db 241 GlnSerGlyArgIleSerIleTyrTrpThrIleValIleProGlyAspIleLeuMetIle 260
QY 810 AACAGTAATGGCAACTAGTTGACCGCGGGGATATTTAAATGAAAACAGGGAAGC 869
Db 261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuLysThrGlyLysSer 280
QY 870 TCTGTAATGAGATCAGATGACCAATGATGATGTTGCTGCTGAATGATATACCAAAAT 929
Db 281 SerValMetArgSerAspAlaProIleAspIleCysValSerGlyCysIleThrProAsn 300
QY 930 GGAAGCATCCCAACGACAAACCAATTTCAAAATGTCGAAACAGTTACATATGAAATGC 989
Db 301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 320
QY 990 CCCAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGATGAGGAATATACAGAA 1049
Db 321 ProLysTyrIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu 340
QY 1050 AAGCAAAATCAGA 1061
Db 341 LysGlnIleArg 344

RESULT 5
Q906N5 O906N5 PRELIMINARY; PRT; 344 AA.
AC Q906N5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hemagglutinin precursor (Fragment).
GN Name=HAI;
OS Influenza A virus (A/equine/Kentucky/1/96 (H3N8)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H3N8 subtype.
OX NCBI_TaxID=217809;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21395169; PubMed=11504416;
RA Lai A.C., Chambers T.M., Holland R.E. Jr., Morley P.S., Haines D.M.,
RA Townsend H.G., Barrandeguy M.;
RT "Diverged evolution of recent equine-2 influenza (H3N8) viruses in the
RT Western Hemisphere.";
RL Arch. Virol. 146:1063-1074(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Lai A.C.K.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Hemagglutinin is responsible for attaching the virus to
CC cell receptors and for initiating infection (By similarity).
CC -!- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
CC (HA1 and HA2) linked by a disulfide bond (By similarity).
CC -!- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
DR EMBL; AF197248; AAF22352.1; -
DR HSSP; P03437; 2VIU.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0019058; P:viral infectious cycle; IEA.
DR InterPro; IPR008980; Capsid Hemag.
DR InterPro; IPR001364; Hemagglutn.
DR InterPro; IPR000149; Hemagglutn. 1.
DR Pfam; PF00509; Hemagglutinin; 1.
DR PRINTS; PR00330; HEMAGGLUTN1.
DR PRINTS; PR00329; HEMAGGLUTN12.
DR ProDom; PD000225; Hemagglutn; 1.
KW Envelope protein; Glycoprotein; Hemagglutinin; Signal.
FT SIGNAL 1 15 potential.
FT CHAIN 16 >344 hemagglutinin.
FT NON_TER 344 344
SQ SEQUENCE 344 AA; 38308 MW; 215ED303718BC710 CRC64;

```

Alignment Scores:

```

Pred. No.: 8.94e-148 Length: 344
Score: 1827.00 Matches: 340
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 98.84% Mismatches: 0
Query Match: 95.55% Indels: 0
DB: 2 Gaps: 0

US-10-826-929a-1 (1-1061) x Q906N5 (1-344)

QY 30 ATGACAGACACCAATATTTGTAATCTACTGACCCCATTTGGTCTACAGTCAAAACCCCAACC 89
Db 1 MetLysThrThrIleIleLeuLeuLeuThrHisIleTrpValTyrSerGlnAsnProThr 20
QY 90 AGTGGAAAACAAACACAGCCACATTTATCTCTGGGACACCATGCGACGTAGCAATGCAATGCAATG 149
Db 21 SerGlyAsnAsnThrAlaThrLeuLysLeuGlyHisAlaValAlaAsnGlyThrLeu 40
QY 150 GTAAAAACAATTAATGATGACCAAAATTTGAGGTGACAAATGCTACTGAAATGATTTAGAGC 209
Db 41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60
QY 210 ATTTCAATAGGGAATATGCAACACTCATATATAAGTTCTAGATGGAAGAAATTCGACA 269
Db 61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr 80
QY 270 TTAATAGATGCAATGCTAGGACACCCCACTGTGATGTTCTCCAGTATGAGAATTTGGAC 329
Db 81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyrGluAsnTrpAsp 100
QY 330 CTCCTCATAGAAGAGCAGCGCTTTTTCAGCAATTTGCTACCCATATGACATCCCTGACTAT 389
Db 101 LeuPheIleGluArgSerAlaPheSerAsnCysTyrProTyrAspIleProAspTyr 120
QY 390 GCATCGCTCGGTCCATTGTAGCATCTCAGGAACATTAGAATTTACAGCAGAGGATTC 449
Db 121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140
QY 450 ACATGGACAGGTGTCTACTCAAACGGAAGTGGAGCGCTGCAAAAGGGGATCAGCCGAT 509
Db 141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysLysArgGlySerAlaAsp 160
QY 510 AGTTCTTTTTCAGCGACTGAATTTGGTGAACAAATTTGGAACCTTTTACCCCATGAAAT 569
Db 161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProThrLeuAsn 180
QY 570 GTGCAATGCTTAAACAAATTTTCGACAACTATACATCTGGGGGATTCATCACCCG 629
Db 181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleTrpGlyIleHisIlePro 200
QY 630 AGCTCAAAACCAACAGCAGACAGATTTGTATCATCCAGAAATCAGGACGAGTAACAGTCTCA 689
Db 201 SerSerAsnGlnLysGlnThrGluLeuTyrIleGlnGluSerGlyArgValThrValSer 220
QY 690 ACAAAGAAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGGTAGGGGT 749
Db 221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProTrpValArgGly 240
QY 750 CAATCAGGCGAGGATAAGCATATATCTGACCAATTTGTAACCTGGAGATATCCTAATGATA 809
Db 241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle 260
QY 810 AACAGTAATGGCAACTAGTTGACCGCGGGGATATTTAAATGAAAACAGGGAAGC 869
Db 261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuLysThrGlyLysSer 280
QY 870 TCTGTAATGAGATCAGATGACCAATGATGATGTTGCTGCTGAATGATATACCAAAAT 929
Db 281 SerValMetArgSerAspAlaProIleAspIleCysValSerGlyCysIleThrProAsn 300
QY 930 GGAAGCATCCCAACGACAAACCAATTTCAAAATGTCGAAACAGTTACATATGAAATGC 989
Db 301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 320

```



Qy	510	AGTTCTTTTAGCCGACTGAATTGCTAAACAAATCTGGAAACTCTTACCCACACTTGAAT	569
Db			
Db	161	Ser-PhePheSerArgLeuAenTrrPLeuThrIysSerGlyAenSerTy-ProThrLeuAen	180
Qy	570	GTGCAGTGGCTTACACATAAATTTTCGCACAACTATACATCTCGGGGATTCATCACCCG	629
Db			
Db	181	ValThrMetProAenAenIysAenPheAspIysLeuTyrlletrpGlylleHishisPro	200
Qy	630	AGGTCACAAACAAACAGACAGACAGATTTGTACATCCAAAGATCAGACAGAGTAACTCTCA	689
Db			
Db	201	SerSerAenGlnGlnThrGluLeuTyrlleGlnGluSerGlyArgValThrValSer	220
Qy	690	ACAAAAAGAGTCAACAAACAGATAGTCCCTAAATATCGGATCTAGACCGTGGGTTAGGGT	749
Db			
Db	221	ThrIysArgSerGlnGlnThrIlelleProAenilleGlySerArgProTrrPValArgGly	240
Qy	750	CAATCAGCGCAGGATAAGCATATATCTGACACCATCTGTAAACCTGGAGATATCCTAATGATA	809
Db			
Db	241	GlnSerGlyArgIleSerIleTyrrtrPThrIleValIysProGlyAspilleuMetIle	260
Qy	810	AACAGTAATGGCAACTTAGTTGACCCCGGGGATATTTTAAATTTGAAAAACAGGAAAAAGC	869
Db			
Db	261	AsnSerAenGlyAenLeuValAlaProArgGlyTyrPheIysLeuIysThrGlyIysSer	280
Qy	870	TCTGTAATGAGATCAGATGCACCATAGACATTTGTGTCTGATCTGAATGTATTACACCAAT	929
Db			
Db	281	SerValMetArgSerAspAlaProIleAspIleCysAlaSerGluCysIleThrProAen	300
Qy	930	GGAAGCATCCCCAACGACAAACCATTTTCAAAATGTGAACAAGTACATATGGAATAATGC	989
Db			
Db	301	GlySerIleProAenAspIysProPheGlnAenValAenIysValThrTyrrGlyIysCys	320
Qy	990	CCCAAGTATATCAGGCCAAACACTTTTAAAGCTGGCCACTGGATGAGGAATATACACGAA	104
Db			
Db	321	ProIysTyrlleArgGlnAenThrLeuIysleuAlaThrGlyMetArgAenValProGlu	340
Qy	1050	AAGCAATCAGA 1061	
Db			
Db	341	LysGlnIleArg 344	
RESULT 8			
OS6858			
ID	OS6858	PRELIMINARY;	PRT; 346 AA.
AC	056858;		
DT	01-JUN-1998 (TrEMBLrel. 06, Created)		
DT	01-JUN-1998 (TrEMBLrel. 06, Last sequence update)		
DE	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Hemagglutinin HA1 subunit precursor (Fragment).		
OS	Influenza A virus (A/equi 2/Bollnas/96(H3N8)).		
OC	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;		
OC	Influenzavirus A; H3N8 subtype.		
OC	NCBI_TaxID=217819;		
RN	[1]		
RA	SEQUENCE FROM N.A.		
RA	Oxburgh L., Akerblom L., Fridberger T., Klingeborn B., Linne T.;		
RN	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RN	SEQUENCE FROM N.A.		
RA	Oxburgh L.H.;		
RA	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.		
CC	-1- FUNCTION: Hemagglutinin is responsible for attaching the virus to		
CC	cell receptors and for initiating infection (By similarity).		
CC	-1- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains		
CC	(HA1 and HA2) linked by a disulfide bond (By similarity).		
CC	-1- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.		
DR	EMBL; Y14060; CAA74388.1; -.		
DR	HSBP; P03437; IEO8.		
DR	GO; GO:0019031; C:viral envelope; IEA.		
DR	GO; GO:0019058; P:viral infectious cycle; IEA.		
DR	InterPro; IPR008980; Capsid hemag.		
DR	InterPro; IPR001364; Hemagglutn.		
DR	InterPro; IPR000149; Hemagglutn.1.		

DR Pfam; PF00509; Hemagglutinin; 1.  
DR PRINTS; PR00330; HEMAGGLUTN1.  
DR PRINTS; PR00329; HEMAGGLUTN12.  
DR ProDom; PD000225; Hemagglutn; 1.  
KW Envelope protein; Glycoprotein; Hemagglutinin; Signal.  
FT SIGNAL 1 16 Potential.  
FT NON TER 346 346  
SQ SEQUENCE 346 AA; 38449 MW; F4755CFF6154C6C9 CRC64;  
Alignment Scores:  
Pred. No.: 2,4e-147 Length: 346  
Score: 1822.00 Matches: 339  
Percent Similarity: 99.71% Conservative: 4  
Best Local Similarity: 98.55% Mismatches: 1  
Query Match: 95.29% Indels: 0  
DB: 2 Gaps: 0  
US-10-826-929A-1 (1-1061) x 056858 (1-346)  
QY 30 ATGAAGACAAACCATTTATTTGATACCTACTACCTACCCCATTTGGGTCTACAGTCAAAACCCAAACC 89  
Db |||||  
1 MetLysThrThrIleLeuLeuLeuLeuLeuHistrpValtyrSerGlnAsnProThr 20  
QY 90 AGTGGAAACACACAGCCACCATTTATCTCTGGACACCATGCGAGTACGAAATGGAACATGTG 149  
Db |||||  
21 SerGlyAsnAsnThrAlaThrLeuLeuLeuGlyHisAlaValAlaAsnGlyThrLeu 40  
QY 150 GTAAAAACATACCTGATGACCAATTTGAGGTGACAAATGCTACTGTAATAGTTCAGAGC 209  
Db |||||  
41 ValLysThrIleThrAsnAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60  
QY 210 ATTTCAATAGGGAATATGCAACATCTCATATAAGTTCTAGATGGAAGAAATGACACA 269  
Db |||||  
61 IleSerIleGlyLysIleCysAsnAsnSerTyArgValLeuAspGlyArgAsnCysThr 80  
QY 270 TTAATAGATGCAATGCTAGGAGACCCCACTGTGTGATCTTCCAGTATGAGAAATGGGAC 329  
Db |||||  
81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyrgluAsnTrpAsp 100  
QY 330 CTCCTCATGAAGAAGAGCCCTTCCAGCAATGCTACCATATGACATCCCTCACTAT 389  
Db |||||  
101 LeuPheIleGluArgSerAlaPheSerAsnCysTyProTyArgPheProAspTy 120  
QY 390 GCATCGCTCCGCTGATGCTAGCATCTCAGGAACATTAAGATTCACAGCAGAGGATTC 449  
Db |||||  
121 AlaSerLeuArgSerIleValIleAspSerGlyThrLeuGluPheThrAlaGluGlyPhe 140  
QY 450 ACATGACAGGTGTCTACTCAAAACGGAAGATGAGCGCTGCAAAAGGGGATCAGCCGAT 509  
Db |||||  
141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysLysArgGlySerAlaAsp 160  
QY 510 AGTTCTTTAGCGGCTGATGGCTTAACAAATCTGGAATCTTACCCACATTCAT 569  
Db |||||  
161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyProThrLeuAsn 180  
QY 570 GTGACAAATCCCTAAACATTAATTCGACAACTATACATCTGGGGATTCATCACCGC 629  
Db |||||  
181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrltrpGlyIleHisHisPro 200  
QY 630 AGCTCAAAACCAACAGACAGAGATTTGTATCCAAAGATCAGGACGAGTAAACAGTCTCA 689  
Db |||||  
201 SerSerAspGlnGlnThrGluLeuTyrlleGlnLysSerGlyArgValThrValSer 220  
QY 690 ACAAAAGAGTCACAAACGATGCTCCCTATATTCGGATCTAGACCGGTAGGGGT 749  
Db |||||  
221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProTrpValArgGly 240  
QY 750 CAATCAGGAGGATAGCATATATCTGACCATTTGTAACACCTGGAGATATCTTAATGATA 809  
Db |||||  
241 GlnSerGlyArgIleSerIleTyTrpThrIleValLysProGlyAspIleLeuMetIle 260  
QY 810 AACAGTAATGGCACTTAGTTGACCGCGGGGATATTTTAATTTGAAACACAGGAAAGC 869  
Db |||||



Db 121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140  
QY 450 ACATGACAGGTGTCTACTCAAAACGAGAAAGTGGAGCTGCAAAAGGGGATCACCCGAT 509  
Db 141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysLysArgGlySerAlaAsp 160  
QY 510 AGTTCTTTAGCCGACTGAATGGCTAACAAATCTGGAATCTTACCCACATTTGAAT 569  
Db 161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTrpProThrLeuAsn 180  
QY 570 GTGCAATGCCCTTAAACAAATTTCCGCAAACTATACATCTGGGGGATTCATCACCG 629  
Db 181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTrpIleTrpGlyLeuHisPro 200  
QY 630 AGCTCAACCAACAGACAGACAGAAATTTGATCCAAAGATCAGGACGAGTAAACGCTCA 689  
Db 201 SetSerAsnAsnGluGlnThrLysLeuTrpIleGlnGluSerGlyArgValThrValSer 220  
QY 690 ACAAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGGTAGGGGT 749  
Db 221 ThrLysArgSerGlnGlnThrIleLeuProAsnLysGlySerArgProTrpValArgGly 240  
QY 750 CAATCAGCAGGATAAGCATATACATACGACCATTTGTAACCTGGAGATATCCTAATGATA 809  
Db 241 GlnSerGlyArgIleSerIleTrpThrIleValLysProGlyAspIleLeuMetIle 260  
QY 810 AACAGTATGGCACTTAGTTCACCGCGGGGATATTTAAATTTGAAACAGGGAAGC 869  
Db 261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTrpPheLysLeuLysThrGlyLysSer 280  
QY 870 TCTGTAATCAGATCAGATCCACCATAGACATTTGTGTCTCGAATGATTTACACCAAT 929  
Db 281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn 300  
QY 930 GGAAGCATCCCCAACACAAACCATTTCAAAATGTGAACAAAGTTACATATGGAATAATGC 989  
Db 301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrgLysCys 320  
QY 990 CCBAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGATATACAGAA 1049  
Db 321 PrbLysTyIleArgGlnLysThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu 340  
QY 1050 AAGCAATCAGA 1061  
Db 341 LysGlnIleArg 344

## RESULT 11

Q67102 PRELIMINARY; PRT; 565 AA.  
AC Q67102;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hemagglutinin precursor.  
GN Name=HA1;  
OS Influenza A virus (strain A/equine/Argentina/1/93).  
OC Viruses; sRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenzavirus A; unidentified subtype.  
OX NCBI\_TaxID=39123;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Equine-2;  
RX MEDLINE=96203953; PubMed=8627254;  
RA Daly J.M., Lai A.C., Binns M.M., Chambers T.M., Barrandeguy M.,  
RA Mumford J.A.;  
RT "Antigenic and genetic evolution of equine H3N8 influenza A viruses.";  
RL J. Gen. Virol. 77:661-671(1996).  
CC -!- FUNCTION: Hemagglutinin is responsible for attaching the virus to  
CC cell receptors and for initiating infection (By similarity).  
CC -!- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains  
CC (HA1 and HA2) linked by a disulfide bond (By similarity).  
CC -!- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.  
DB EMBL; L39913; AAB36975.1; -.

DR HSP; P03437; 10U1.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0019038; P:viral infectious cycle; IEA.  
DR InterPro; IPR00980; Capsid hemag.  
DR InterPro; IPR001364; Hemagglutn.  
DR InterPro; IPR001149; Hemagglutn.1.  
DR Pfam; PF00509; Hemagglutinin; 1.  
DR PRINTS; PR00330; HEMAGGLUTN1.  
DR PRINTS; PR00329; HEMAGGLUTN12.  
DR ProDom; PD000225; Hemagglutn; 1.  
KW Envelope protein; Glycoprotein; Hemagglutinin; Signal.  
FT SIGNAL 1 15 Potential.  
FT CHAIN 16 344 hemagglutinin.  
FT CHAIN 16 565 hemagglutinin.  
SQ SEQUENCE 565 AA; 63714 MW; 13135C9B04CC560D CRC64;

## Alignment Scores:

Pred. No.: 1,51e-146 Length: 565  
Score: 1813.00 Matches: 337  
Percent Similarity: 99.42% Conservative: 5  
Best Local Similarity: 97.97% Mismatches: 2  
Query Match: 94.82% Indels: 0  
DB: 2 Gaps: 0

US-10-826-929A-1 (1-1061) x Q67102 (1-565)

QY 30 ATGAGACAAACATATTTTGTATCTACTGACCATTTGGTCTCAGTCACAAACCCACACC 89  
Db 1 MetLysThrThrIleLeuLeuLeuThrHisTrpValTySerGlnAsnProThr 20  
QY 90 AGTGAACAACAACAGACACCATTTATGCTCTGGGACACCATCGCAGTAGCAAAATGGAAACATTG 149  
Db 21 SerGlyAsnAsnThrAlaThrLeuLysLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40  
QY 150 GTAAAAACAATPACTGATGACAAATAGAGTGACAAATGTCTAGTAATAGTTAGTTCAGAGC 209  
Db 41 VallysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60  
QY 210 ATTTCAATAGGAAATATGCAACACTCATATAAGTTCTAGATGGAGAAATGGACACA 269  
Db 61 IleSerIleGlyLysIleCysAsnAsnSerTyArgValLeuAspGlyArgAsnCysThr 80  
QY 270 TTAATAGATGCAATGCTAGGAGACCCCATCTGTATGTCTTCCAGTATGAGAATTTGGGAC 329  
Db 81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyThrGluAsnTrpAsp 100  
QY 330 CTCTTCATAGAAAGAGCAGCGCTTTACGAAATTTGCTACCCATATGACATCCCTGACTAT 389  
Db 101 LeuPheIleGluArgSerSerAlaPheSerAsnCysTyProTyAspIleProAspTy 120  
QY 390 GCATCGCTCCGTCCTCCTAGCATCTCCGGAACATTAGAATTCACAGCAGAGGGATTC 449  
Db 121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140  
QY 450 ACATGACAGGTGTCTACTCAAAACGAGAAAGTGGAGCTGCAAAAGGGGATCACCCGAT 509  
Db 141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysLysArgGlySerAlaAsp 160  
QY 510 AGTTCTTTAGCCGACTGAATGGCTAACAAATCTGGAATCTTACCCACATTTGAAT 569  
Db 161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyProThrLeuAsn 180  
QY 570 GTGCAATGCCCTTAAACAAATTTCCGCAAACTATACATCTGGGGGATTCATCACCG 629  
Db 181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTrpIleTrpGlyLeuHisPro 200  
QY 630 AGCTCAACCAACAGACAGACAGAAATTTGATCCAAAGATCAGGACGAGTAAACGCTCA 689  
Db 201 SerSerAsnAsnGlnGlnThrLysLeuTrpIleGlnGluSerGlyArgValThrValSer 220  
QY 690 ACAAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCAGGACCGTGGGTAGGGGT 749  
Db 221 ThrLysArgSerGlnGlnThrIleLeuProAsnLysGlySerArgProTrpValArgGly 240





```

RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Equine-2; PubMed=8627254;
RX  MEDLINE=96203953;
RA  Daly J.M., Lai A.C., Binns M.M., Chambers T.M., Barrandeguy M.,
RA  Mumford J.A.;
RT  "Antigenic and genetic evolution of equine H3N8 influenza A viruses.";
RL  J. Gen. Virol. 77:661-671(1996).
CC  -1- FUNCTION: Hemagglutinin is responsible for attaching the virus to
CC  cell receptors and for initiating infection (By similarity).
CC  -1- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
CC  (HA1 and HA2) linked by a disulfide bond (By similarity).
CC  -1- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
DR  EMBL; L39917; AAB36979.1; -.
DR  HSSP; P03437; 1QUL.
DR  GO; GO:0019058; P:Viral infectious cycle; IEA.
DR  InterPro; IPR008980; Capsid_hemag.
DR  InterPro; IPR001364; Hemagglutn.
DR  InterPro; IPR000149; Hemagglutn_1.
DR  Pfam; PF00509; Hemagglutinin; 1.
DR  PRINTS; PR00330; HEMAGGLUTN1.
DR  PRINTS; PR00329; HEMAGGLUTN12.
DR  ProDom; PD000225; Hemagglutn; 1.
KW  Envelope protein; Glycoprotein; Hemagglutinin; Signal.
FT  SIGNAL 1 15 potential.
FT  CHAIN 16 344 hemagglutinin.
FT  CHAIN 16 565 hemagglutinin.
FT  FT CHAIN 16 565 hemagglutinin.
SQ  SEQUENCE 565 AA; 63770 MW; 8453CC658EADC80F CRC64;

Alignment Scores:
Pred. No.: 2,72e-146 Length: 565
Score: 1810.00 Matches: 335
Percent Similarity: 99.71% Conservative: 8
Best Local Similarity: 97.38% Mismatches: 1
Query Match: 94.67% Indels: 0
DB: 2 Gaps: 0

US-10-826-929A-1 (1-1061) x Q67106 (1-565)
QY 30 ATGACGACACCAATTTTGTACTACTGACCCATTGGGTCTACAGTCAAAACCCAAAC 89
DB 1 MetLysThrThrIleLeuIleLeuLeuThrHisTrpValTrpSerGlnAsnProThr 20
QY 90 AGTGGAAACACACAGCCACATTATGCTGGGACACCATGTCAGTACCAATGAACATTG 149
DB 21 SerGlyAsnAsnThrAlaThrLeuLeuLeuGlyHisAlaValAlaAsnGlyThrLeu 40
QY 150 GTAAACCAATACTGATGACCAAAATGAGGTGACAAATGCTACTGAATTTAGTTCAGAC 209
DB 41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60
QY 210 ATTTCAATGCGGAAATATGCAACAACACTATATAAGTTCTAGATCGAAGAAATTCACA 269
DB 61 IleSerIleGlyLysIleCysAsnAsnSerTrpArgValLeuAspGlyArgAsnCysThr 80
QY 270 TTAATAGATCAATGCTAGGAGACCCCACTGATGTCTCCAGTATGAGATTCGGAC 329
DB 81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTrpGluAsnTrpAsp 100
QY 330 CTCTTCATGAAAGACGCGCTTTTCAGCAATTTGCTACCCATATGACATCCCTGACTAT 389
DB 101 LeuPheIleGluArgSerAlaPheSerAsnCysTrpProTrpAspIleProAspTrp 120
QY 390 GCATCGCTCGGTCCATTTAGCATCTCTAGGAACATTTAGAAATTCACAGAGGATTC 449
DB 121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140
QY 450 ACATGACACGGTCTCACTCAAAACGGAAGTGGAGCTGCAAAAGGGGATCAGCCGAT 509
DB 141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysLysArgGlySerAlaAsp 160
QY 510 AGTTTCTTTAGCGGACTGAATTTGGCTTAAACAAATCTGGAACCTTTACCCACATTGAAT 569

```

```

DB 161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTrpProThrLeuAsn 180
QY 570 GTGACAAATGCCTAAACAATAAAATTTTCGACAAACTATACATCTGGGGGATTCATCACCCG 629
DB 181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTrpIleTrpGlyLeuHisHisPro 200
QY 630 AGCTCAAACCAACAGCAGACAGCAATTTGTATCATCTCAAGAAATCAGGACGAGTAAACAGTCTCA 689
DB 201 SerSerAsnAsnGluGlnThrLysLeuTrpIleGlnGluThrGlyArgValThrValSer 220
QY 690 ACAAAAAGAGTCAACAACAGTATAGTCCCTATATCCGATCTAGACCGTGGGTAGGGT 749
DB 221 ThrLysArgSerGlnGlnThrIleLeuProAsnIleGlySerArgProTrpValArgGly 240
QY 750 CAATCAGCGCAGGATAGCATATCTGACCATTTGTAACCACTGGAGATATCTTAATGATA 809
DB 241 GlnSerGlyArgIleSerIleTrpThrIleValLysProGlyAspIleLeuMetIle 260
QY 810 AACAGTAATGGCAACTTAGTTCACCGCGGGGATATTTTAAATTTGAAATCAGGAAAGC 869
DB 261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTrpPheLysLeuArgThrGlyArgSer 280
QY 870 TCTGTAATGATGATCAGATCCACCCATAGACATTTGCTCTCGAATGTATTACACAAAT 929
DB 281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn 300
QY 930 GGAAGCATCCCAACGACAAACCATTTTCAAAATGTGAACAAAGTTACATATGAAATGC 989
DB 301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTrpGlyLysCys 320
QY 990 CCCAAGTATATCAGGCAAAACACTTTTAAAGCTGGCCACTGGGATGAGGATATACAGAA 1049
DB 321 ProLysTrpIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu 340
QY 1050 AAGCAAAATCAGA 1061
DB 341 LysGlnIleArg 344

RESULT 15
Q906N8 PRELIMINARY; PRT; 344 AA.
AC Q906N8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
DE Hemagglutinin precursor (Fragment).
GN Name=HA1;
OS Influenza A virus (A/equine/Argentina/2/94 (H3N8)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H3N8 subtype.
OX NCBI_TaxID=217812;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21395169; PubMed=11504416;
RA Lai A.C., Chambers T.M., Holland R.E. Jr., Morley P.S., Haines D.M.,
RA Townesend H.G., Barrandeguy M.;
RT "Diverged evolution of recent equine-2 influenza (H3N8) viruses in the
RT Western Hemisphere.";
RL Arch. Virol. 146:1063-1074 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Lai A.C.K.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Hemagglutinin is responsible for attaching the virus to
CC cell receptors and for initiating infection (By similarity).
CC -1- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
CC (HA1 and HA2) linked by a disulfide bond (By similarity).
CC -1- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
DR EMBL; AF197245; AAF22349.1; -.
DR HSSP; P03437; 2VIU.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR008980; Capsid_hemag.

```



Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	44.6	4.2	878	9	CNS01087R	AL108993 Drosophil
2	43.8	4.1	598	8	AQ636729	AQ636729 RPC1-11-4
3	43.8	4.1	820	8	CC081372	CC081372 CSU-K33r.
4	42.8	4.0	854	9	CNS00090X	AL052980 Drosophil
5	42.4	4.0	1101	9	CNS0106X	AL098595 Drosophil
6	42	4.0	665	6	BY725844	BY725844 Drosophil
7	41.6	3.9	1106	9	CNS000LRE	AL078654 Drosophil
8	41.4	3.9	733	8	AQ055729	AQ055729 CIT-HSP-2
9	41	3.9	1101	9	CNS00086Y	AL073010 Drosophil
10	41	3.9	1362	9	AG429915	AG429915 Mus muscu
11	40.8	3.8	879	5	EX6933295	EX6933295 BX63295
12	40.8	3.8	1342	9	CL650318	CL650318 CH213-288
13	40.6	3.8	503	8	BH744818	BH744818 qt42d05_b
14	40.6	3.8	543	7	CK563338	CK563338 zswpb0_00
15	40.6	3.8	968	9	CNS01172G	AL07506 Drosophil
16	40.4	3.8	610	8	AZ345336	AZ345336 IM0079P14
17	40.4	3.8	1005	9	CNS0007DD	AL067043 Drosophil
18	40.2	3.8	470	7	CK747765	CK747765 nad03-4cs
19	39.8	3.8	1101	9	CNS000LT2	AL078714 Drosophil
20	39.8	3.8	1400	9	AG430154	Mus muscu
21	39.6	3.7	1011	3	CNS008YXN	BX030807 Single re
22	39.4	3.7	498	8	AZ026564	AZ026564 RPC1-23-3
23	39.4	3.7	558	8	AZ400010	AZ400010 IM0166B12
24	39.4	3.7	687	5	BQ476807	BQ476807 meladema2



QY	956	TCAAAATGTGACAAAGTTTACATATGCGAAAATGCCCCCAAGTATATCATCAGGCACAAACACTTTT	1015
Dd	209	NNNNNANNAANAANNNNNNNAAAAAANNNNNNNAANAAAAAANNNNNNANN	150
QY	1016	AAGCTTGCCACTGGGATGAGGAATATACCAGAAAAGCAA	1056
Dd	149	NNNNCADVKAACCAAAAGGAAAAAANNNNNNAAAAABAA	109

  

RESULT 5	CNS0106X	linear	GSS 26-JUL-1999
LOCUS	CNS0106X	1101 bp	DNA
DEFINITION	Drosophila melanogaster genome survey sequence T7 end of BAC BACN03K20 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.		
ACCESSION	AL098595		
VERSION	AL098595.1	GI:5610206	
KEYWORDS	GSS.		
SOURCE	Drosophila melanogaster (fruit fly)		
ORGANISM	Drosophila melanogaster		
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
REFERENCE	1 (bases 1 to 1101) Genoscope.		
AUTHORS	Direct Submission		
TITLE	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :		
JOURNAL	BP 191 9106 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		
COMMENT	- Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) -		

```

http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES             Location/Qualifiers
     source            1..1101
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACN03K20"
                     /clone_lib="DroebAC"
                     /plasmid="pbelobAC11"
                     /note="end : T7"

ORIGIN
Query Match          4.0%; Score 42.4; DB 9; Length 1101;
Best Local Similarity 19.3%; Pred.No. 3;
Matches 67; Conservative 140; Mismatches 141; Indels 0; Gaps 0;

QY    563 ATTGAATGTGACAATGCCTAACCAATAAAAAATTTCGACAAACTATACATCTGGGGGATTC A   622
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db    754 RDKRWDAKDKRKAARAKAADAADDAADAKDAKAADAKADAADDDGRGDGKKRA   813

QY    623 TCACCCGAGTCAAACCACAGCAGACAGNAATTGTATCATCCAGAATCAGGACGAGTTAC   682
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db    814 KDRKKKKKKDKAWGDKKKAKDKAAAKADAADAGDAKARRRAGDGKDAKADAKAAKKAK   873

QY    683 AGTCTCAACAAAAGAAGTCAACAAAACGATAGTGCCCTAATATCGGATCTAGACCGTGGGT   742
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db    874 AKDDDDAKATTAATKATTAKKDKAKAKKKKKKKDKDAKAKAKADAKDKDDKDDKDKK   933

QY    743 TAGGGGTCAATCAGGCAGGATAGCATATATCTGGACCATTTGTAAAAACCTGGAGATATCT   802
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db    934 DAKADKKKKDKRAKDAKKDDPKDKANDKDKDADAKADAKADAKADADAKAKAKAKA   993

QY    803 AATGATAAACAGTAATGGCACTTAGTTGCCCGCGGGGATATTTTAAATTGAAAACAGG   862
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db    994 KAADDDAAAADAKAADADAKAKAKADAAKAKADAKADAKADADAKAKAAKRAKAKADA   1053

```

QY 863 GAAAGCTCTGTAATGAGATGAGATGACCCATAGACATTGTGTGTC 910  
Db 1054 DAAKAKAKADKKDKAKKADADRAKAKAKADAKAKAKAKAKAKDM 1101

RESULT 6  
BY725844  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BY725844 665 bp mRNA linear EST 17-DEC-2002  
BY725844 RIKEN full-length enriched, 2 cells egg Mus musculus cDNA  
clone B020021A19 5', mRNA sequence.  
BY725844  
EST.  
BY725844.1 GI:27138971  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 665)  
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,  
Kiyosawa, H., Tagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,  
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,  
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusci, V.,  
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,  
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,  
Cariboldi, S., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,  
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,  
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,  
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,  
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,  
Numata, K., Okido, T., Pavan, W.J., Perlea, G., Pesole, G.,  
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,  
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,  
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,  
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,  
Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y.,  
Wells, C., Wilming, L.G., Wyshaw-Boris, A., Yanagisawa, M., Yang, I.,  
Yang, L., Yuan, Z., Zvolan, M., Zhu, Y., Zimmer, A., Carninci, P.,  
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,  
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,  
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,  
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,  
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,  
Rogers, J., Birney, E. and Hayashizaki, Y.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
22354683  
12466851  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,  
Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,  
Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,  
Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,  
Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,  
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, W.,  
Takeda, Y., Waki, K., Watanishi, A., Muramatsu, M. and Hayashizaki, Y.  
Direct Submission  
Computational Analysis of Full-Length Mouse cDNAs Compared with  
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site (http://genome.gsc.riken.go.jp) for  
further details.  
Location/Qualifiers  
1. 665  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="B020021A19"  
/tissue type="egg"  
/dev stage="2 cells"  
/lab\_host="DH10B"  
/clone\_lib="RIKEN full-length enriched, 2 cells egg"  
/note="Site 1: Sali; Site 2: BamHI; cDNA library was  
prepared and sequenced in Mouse Genome Encyclopedia  
Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN. Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer [5'  
GAGAGAGAGAGAGTCCAGAGCTCTTTTCTTTTCTTTTCTTTT 3'], cDNA was  
prepared by using trehalose thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trapper. Second strand cDNA was prepared with the  
primer adapter of sequence [5'  
GAGAGAGAGATCTCGAGTAATTAATTAATTCCTCCCCCCCC 3']. cDNA  
was cleaved with XhoI and BamHI. Vector: a modified  
pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN  
Query Match 4.0%; Score 42; DB 6; Length 665;  
Best Local Similarity 50.0%; Pred. No. 3.3; Mismatches 0; Gaps 0;  
Matches 105; Conservative 0; Indels 105; Indels 0;  
QY 819 GGCACCTTAGTTGCACCGCGGGATATTTAAATTTGAAACACAGGAAAGCTCTCTAATG 878  
Db 177 GACAAACCAATGAATGCTGTGTTCACTCATGTGCCAGAGGTGGAACTCGACCCAT 236  
QY 879 AGATCAGATGACCCATAGACATTTGTGTGCTGAATGTTATACACCAATGGAAGCATC 938  
Db 237 ATATCTCATCCACCTGACAAATTAATTGATTCAGAAATGATCAGCCCATTCATAGAAGA 296  
QY 939 CCCACGACAAACCACTTTCAAAATGTGAACAAAGTTACATATGGAATGCCCAAGTAT 998  
Db 297 CCAGAAGCTCTGAAACTGAGATGAGAACAAAGAAATTAATGCTAGATAGATTATGAAA 356  
QY 999 ATCAGGCAAAACACATTTTAAAGCTGCCACT 1028  
Db 357 AGGACTCCAGGAATTTAGTGTGTGTCATT 386

RESULT 7  
CNS00LRE/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CNS00LRE 1106 bp DNA linear GSS 14-JUN-1999  
Drosophila melanogaster genome survey sequence T7 end of BAC:  
BACR48P05 of RPCI-98 library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.  
AL078654  
AL078654.1 GI:5101944  
GSS.  
Drosophila melanogaster (fruit fly)  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1106)  
 AUTHORS Genoscope.  
 TITLE Direct Submission  
 JOURNAL Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Peter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial, EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES  
 source Location/Qualifiers  
 1..1106  
 /organism="Drosophila melanogaster"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7227"  
 /clone="BACR48P05"  
 /clone\_lib="RPCI-98"  
 /note="end : T7"

ORIGIN  
 Query Match 3.9%; Score 41.6; DB 9; Length 1106;  
 Best Local Similarity 15.4%; Pred. No. 5;  
 Matches 55; Conservative 151; Mismatches 152; Indels 0; Gaps 0;

QY 588 AAAAAATTCGACAACTATACATCTGGGGATTCATCACCGGAGTCAACACGAG 647  
 ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||  
 Db 1041 AHKDKRSKKBDDGVNTWADNTBWSRRHNCVRBDSVMVHAWVTDYBCRCNTYK 982

QY 648 ACAGAAATTCGACAACTACGAGCAGGATTAACAGTCTCAACAAAGAAAGTCAACA 707  
 ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||  
 Db 981 VSKWBTBKHYVNBCKYKBWHAAWAAWAAADCCCRBRWAVAWAAWAAWMAA 922

QY 708 ACGATAGTCCCTAATATCGGATCTAGACCGTGGTGGTGGTGGTGGTGGTGGTGGT 767  
 ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||  
 Db 921 MKHTSGBKYSYDMHTKYKWKHWWYKSGNGSGSGSVWVWCMRHAYTHRWVWY 862

QY 768 ATATCTGACACCTGTAACCTCGAGATATCCTAATGATTAACAGTAACTGCGCACT 827  
 ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||  
 Db 861 NWWBDSGBVCMCCVMAHCAHBMVHCYTYNAMSCANBAWYVAVKSBTRTHAWN 802

QY 828 GTTGACCCGCGGGATATTTAAATGAAACACAGGAAAGCTCTGTAATGATGAT 887  
 ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||  
 Db 801 ANGTWAKSGSGCACCSGMRHYTGGRARSRGKMGVCCVKBMWHAHBNHNNY 742

QY 888 GCACCCATGACATTTGTGTGTGCTGATGATTTATACCAAAATGGAAGCATCCCA 945  
 ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||  
 Db 741 NNMAWAAVAMNNWATKYKKNACYKKTGDVAYMBAVARSVRVNCVAVAVABG 684

RESULT 8  
 AQ055729/c 733 bp DNA linear GSS 30-JUL-1998  
 LOCUS CIT-HSP-2341D11.TF CIT-HSP Homo sapiens genomic clone 2341D11,  
 DEFINITION genomic survey sequence.

ACCESSION AQ055729  
 VERSION AQ055729.1 GI:3352335  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 733)

AUTHORS Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M., and Venter, J.C.  
 TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)  
 JOURNAL Unpublished (1998)  
 COMMENT Other GSSs: CIT-HSP-2341D11.TR  
 Contact: Mark Adams  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: mdadams@tigr.org  
 Clones are available from Research Genetics (info@resgen.com). BAC end search page:  
[http://www.tigr.org/tldb/hungen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html).  
 Seq primer: M13-21  
 Class: BAC ends.

FEATURES  
 source Location/Qualifiers  
 1..733  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clone="2341D11"  
 /sex="Male"  
 /cell\_type="Sperm"  
 /clone\_lib="CIT-HSP"  
 /note="Vector: pBelobAC11; Site\_1: HindIII; Site\_2: HindIII"

ORIGIN  
 Query Match 3.9%; Score 41.4; DB 8; Length 733;  
 Best Local Similarity 53.4%; Pred. No. 5;  
 Matches 87; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 129 GCAGTAGCAATGGAACATTTGGTAAACAACTAATCTGATGACCAATGAGGTGCAAAAT 188  
 ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||  
 Db 469 GCAGCAGGAATGAAATGATAGATTAAATTAAGAGAGAGAAAATATCAATAGTAGTT 410

QY 189 GCTACTGATGATTTGTCAGAGCATTTCAATAGGAAAAATGCAACACTCATATAAGTT 248  
 ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||  
 Db 409 TAAATAAATATGTTTCAGAAAATCTGAAGGGTAAATAATGAATAATCCATAAAGGAA 350

QY 249 CTGATGCGAAGAAATTCACATTAATAGATCAATGCTAGGAG 291  
 ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||  
 Db 349 CAAGAAATTAATGAACTAAAGCAGATTAAATGAATAATAAAG 307

RESULT 9  
 CDS00H6Y 1101 bp DNA linear GSS 03-JUN-1999  
 LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC:  
 BACR34101 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

DEFINITION AL073010  
 AL073010.1 GI:4952872  
 GSS.  
 Drosophila melanogaster (fruit fly)  
 Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 1101)  
 Genoscope.  
 Direct Submission  
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
 Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information





Tel: 516 367 8884  
 Fax: 516 367 8874  
 Email: mcombie@cshl.org  
 Plate: gt42 row: d column: 05  
 Seq primer: -21UnivFwd  
 Class: shotgun  
 High quality sequence stop: 503.

# FEATURES

Location/Qualifiers  
 1. .503  
 /organism="Brassica oleracea"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:3712"  
 /clone="gt42d05"  
 /clone\_lib="BosBud01"  
 /note="Vector: M13 for .x reads, pBluescript for .b and .g reads; Site 1: EcoRV; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO100DH3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA provided by Pablo Rabinowicz (CSHL) and shotgun library prepared in McCombie Lab."

## ORIGIN

Query Match 3.8%; Score 40.6; DB 8; Length 503;  
 Best Local Similarity 58.8%; Pred. No. 7.4;  
 Matches 70; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 187 ATGCTACTGAATTGCTAGAGCATTTCAATGAGGAAATATGCAACACTCATATAAG 246  
 Db 365 ATGGCTTGAATTACCTGTGATTATTCATATAGTGAAGAGATCTAGAGTAAGATCCAG 424

QY 247 TTCTAGATGGAGAATTCCATTAATAGATGCAATGCTAGGACCCCACTGTAT 305  
 Db 425 CTAAAAAGGAAAGATAGAACATTCAGACATGAAAGTCTAGGAGGAACAACTTTAT 483

## RESULT 14

CK563538/c  
 LOCUS 643 bp, mRNA linear EST 05-OCT-2004  
 DEFINITION rswb0\_006755.y1 swp Bombyx mori cDNA, mRNA sequence.  
 ACCESSION CK563538  
 VERSION CK563538.1 GI:40947992  
 KEYWORDS EST.  
 SOURCE Bombyx mori (domestic silkworm)  
 ORGANISM Bombyx mori  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyx.

## REFERENCE

AUTHORS Xia Q., Zhou Z., Lu C., Cheng D., Dai F., Li B., Zhao P., Zha X., Cheng T., Chai C., Pan G., Xu J., Liu C., Lin Y., Qian J., Hou Y., Wu Z., Li G., Pan M., Li C., Shen Y., Lan X., Yuan L., Li T., Xu H., Wang G., Wan Y., Zhu Y., Yu M., Shen W., Wu D., Xiang Z., Yu J., Wang J., Li R. Q., Shi J. P., Li H., Li G. Y., Su J. N., Wang X. L., Li G. Q., Zhang J. J., Wu Q. F., Li J., Zhang Q. P., Wei N., Xu J. Z., Sun H. B., Dong L., Liu D. Y., Zhao S. L., Zhao X. L., Meng Q. S., Lan F. D., Huang X. G., Li Y. Z., Fang F., Li C. F., Li D. W., Sun Y. Q., Zhang Z. P., Yang Z., Huang Y. Q., Xi Y., Qi Q. H., He D. D., Huang H. Y., Zhang X. W., Wang Z. Q., Li W. J., Cao Y. Z., Wang J., Ye J., Ji H., Li S. T., Ni P. X., Zhang J. G., Zhang Y., Zhang H. K., Ye C., Wang J., Wong G. K. S., and Yang H. M.

A draft sequence for the genome of the domesticated silkworm (Bombyx mori)

## TITLE

Unpublished (2004)  
 Contact: Zhonghui Xiang  
 Southwest Agricultural University  
 Chongqing Beibei  
 Tel: 86-23-68251123  
 Fax: 86-23-68251128  
 Email: xzh@swau.cq.cn.  
 Location/Qualifiers  
 1. .643  
 /organism="Bombyx mori"

## FEATURES

source

/mol\_type="mRNA"  
 /strain="DaZhao (P50)"  
 /db\_xref="taxon:7091"  
 /sex="mixed"  
 /dev\_stage="Embryo (unfertilized)"  
 /clone\_lib="swp"  
 /note="Vector: pBluescript II SK(+)"

## ORIGIN

Query Match 3.8%; Score 40.6; DB 7; Length 643;  
 Best Local Similarity 50.3%; Pred. No. 8;  
 Matches 100; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 463 TCACCTCAAAAGGGAAGTGGAGCGCTGCAAAAGGGGATCAGCCGATAGTTCTTTAGCC 522  
 Db 375 TAACCTAATAGGAAGGCTTAACACATAAATAATGGGATATCTATTTTATTGTCA 316

QY 523 GACTGAATTGCTTAACAAAATCTGAAACCTTACCCCACTGAATGTGACAATGCTA 582  
 Db 315 CCTTAACCTTTACAAACAAATCCATAATATATAAGGCCACTTTTTTTTCAACAATACAC 256

QY 583 ACAATAAAATTTTCGACAACTATACATCTCTGGGGATTCATCACCAGCTCAACCAAC 642  
 Db 255 TAAGTTAGACTGGTGAATGACCTGCTTGCAGTTAAGTGGTTATCTGAGCCCAATAACAT 196

QY 643 AGCAGACAGAAATTTGACAT 661  
 Db 195 TGCAATGGAATGTACCT 177

## RESULT 15

CNS0172G  
 LOCUS 968 bp, DNA linear GSS 26-JUL-1999  
 DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC BACN17B23 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

## ACCESSION

VERSION AL107506.1 GI:5627693

## KEYWORDS

GSS.

## SOURCE

ORGANISM Drosophila melanogaster (fruit fly)  
 Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyroidae; Drosophilidae; Drosophila.

## REFERENCE

1 (bases 1 to 968)

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Genoscope.  
 Direct Submission  
 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)  
 - Web : www.genoscope.cns.fr  
 Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.

## FEATURES

## source

Location/Qualifiers  
 1. .968  
 /organism="Drosophila melanogaster"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7227"  
 /clone="BACN17B23"  
 /clone\_lib="DrosBAC"  
 /plasmid="pBeloBAC11"  
 /note="end : SP6"

## ORIGIN

Query Match 3.8%; Score 40.6; DB 9; Length 968;  
 Best Local Similarity 36.2%; Pred. No. 9;  
 Matches 59; Conservative 39; Mismatches 65; Indels 0; Gaps 0;

Qy 129 GCAGTAGCAAAATCGAACATTGGTAAACAAATTAACCTGATGACCAAAATTGAGGTGACAAAT 188  
Db 738 GAAAGAGKAAAAGKRAAAAAGAGAAAAGABRAGGERARAKKAAKAAKKAKAKTAAB 797  
Qy 189 GCTACTGAATTAGTTTCAGAGCATTTCAATAGGGGAAAATATGCAACAACCTCATATAAGTT 248  
Db 798 KAKAADAAKKRKATGAKADAKAKKADKADAKADAKADAKADAKADAKADAKAKSACK 857  
Qy 249 CTAGATGGAAAGAAATTGCACATTAAATAGATGCAATGCTAGGAG 291  
Db 858 AAAAAAAAAAAATGAAAAATAAAAAANGAAKAKSWGTGTG 900

Search completed: March 1, 2005, 06:14:30  
Job time : 4086 secs

**This Page Blank (uspto)**